

OY 293 FHCCINPLIYAFAGKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSSPHSS 352
 DB 301 FHCCINPLIYAFAGKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSSPHSS 360

RESULT 2
 ID 077488 PRELIMINARY: PRT: 352 AA.
 AC 077488.

DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DE CXC4 RECEPTOR.
 OS Cercopithecus aethiops (Green monkey) (Griwet).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;
 DE Chlorocebus.

RA [1]
 RA SEQUENCE FROM N.A.
 RA MURAYAMA Y., MATSUNAGA S., INOUE-MURAYAMA M.;
 RT "cDNA sequence of African green monkey CXC4-4 chemokine receptor
 gene.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AB015943; BAA31327.1; -.
 DR PFAM: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 SQ SEQUENCE 352 AA; 39773 MW; BD05150 CRC32;

Query Match 98.7%; Score 1806; DB 6; Length 352;
 Best Local Similarity 98.6%; Pred. No. 1,4e-137;
 Matches 347; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 MEGISITSDNTYEMSGDYSKMKPCFRENANFNKIFLPTIYSIIFLTGIVNGLYI 60
 DB 1 MEGISITSDNTYEMSGDYSKMKPCFRENANFNKIFLPTIYSIIFLTGIVNGLYI 60
 OY 61 LVMGYSOKLRMTDKYRLHLVSADLLFVITLPFWAVDAVANWYFGNLCRAVHYITVNL 120
 DB 61 LVMGYSOKLRMTDKYRLHLVSADLLFVITLPFWAVDAVANWYFGNLCRAVHYITVNL 120
 OY 121 YSSVLLIATISIDRYLATIYHATNSQPRKLAEKVYVGVWIPALLITPDIPIANVSEA 180
 DB 121 YSSVLLIATISIDRYLATIYHATNSQPRKLAEKVYVGVWIPALLITPDIPIANVSEA 180
 OY 181 DORYICDRYPNDLWVYVFOQHIMVGLIPGIVILSCYCIITISKLSHGKQRKALKT 240
 DB 181 DORYICDRYPNDLWVYVFOQHIMVGLIPGIVILSCYCIITISKLSHGKQRKALKT 240
 OY 241 TVILLIAFACWLPYIIGISIDSFILLEITIKOGCEPENTVHKWISTEALAFHCCCLNPI 300
 DB 241 TVILLIAFACWLPYIIGISIDSFILLEITIKOGCEPENTVHKWISTEALAFHCCCLNPI 300
 OY 301 LYAFIAGAKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSSPHSS 352
 DB 301 LYAFIAGAKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSSPHSS 352

RESULT 3
 ID 062973 PRELIMINARY: PRT: 332 AA.
 AC 062973.

DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE CHEMOKINE RECEPTOR (LCRI).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RA WONG M., XIN W.W., DUMAN R.S.;
 RL Mol. Psych. 0:0-0(0).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: U54791; AAB01981.1; -.
 DR PFAM: PF00001; 7tm_1; 2.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 SQ SEQUENCE 332 AA; 37442 MW; C0EAB84B CRC32;

Query Match 84.6%; Score 1548.5; DB 11; Length 332;
 Best Local Similarity 86.0%; Pred. No. 6.1e-117;
 Matches 300; Conservative 16; Mismatches 16; Indels 17; Gaps 2;

OY 4 ISITYSDNTYEMSGDYSKMKPCFRENANFNKIFLPTIYSIIFLTGIVNGLYI 63
 DB 1 MEITYSDNTYSEVSGDYSKMKPCFRENANFNKIFLPTIYSIIFLTGIVNGLYI 60
 OY 64 GYOKLRMTDKYRLHLVSADLLFVITLPFWAVDAVANWYFGNLCRAVHYITVNL 123
 DB 61 GYOKLRMTDKYRLHLVSADLLFVITLPFWAVDAVANWYFGNLCRAVHYITVNL 118
 OY 124 VLLIAFISLDRIYLAIVHATNSQPRKLAEKVYVGVWIPALLITPDIPIANVSEADDR 183
 DB 119 VLLIAFISLDRIYLAIVHATNSQPRKLAEKVYVGVWIPALLITPDIPIANVSEADDR 163
 OY 184 YICDRFYNDLWVYVFOQHIMVGLIPGIVILSCYCIITISKLSHGKQRKALKT 243
 DB 164 YICDRFYNDLWVYVFOQHIMVGLIPGIVILSCYCIITISKLSHGKQRKALKT 223
 OY 244 LIAFACWLPYIIGISIDSFILLEITIKOGCEPENTVHKWISTEALAFHCCCLNPI 303
 DB 224 LIAFACWLPYIIGISIDSFILLEITIKOGCEPENTVHKWISTEALAFHCCCLNPI 283
 OY 304 FLGAKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSSPHSS 352
 DB 284 FLGAKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSSPHSS 332

RESULT 4
 ID 09YGC3 PRELIMINARY: PRT: 358 AA.
 AC 09YGC3.

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE CHEMOKINE RECEPTOR 4.
 GN CXC4.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia; Anura;
 OC Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.
 RN [1]

RP SEQUENCE FROM N.A.
 RA MOERPS B., KNOEPFLE K., BROWN M., KNOEHEL W., GIERSCHIK P.;
 RT "Expression of the CXC chemokine receptor 4 during early Xenopus
 laevis embryogenesis: a possible role of chemokine receptors as
 regulators of development and differentiation.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: Y17895; CAA76924.1; -.
 DR EMBL: Y17894; CAA76923.1; -.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
 KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
 SQ SEQUENCE 358 AA; 40078 MW; E991FDID CRC32;

Query Match 75.7%; Score 1386; DB 13; Length 358;
 Best Local Similarity 75.1%; Pred. No. 7.1e-104;

	Matches	265;	Conservative	36;	Mismatches	48;	Indels	4;	Gaps	2.
OY	3	GISITSDNYTEEMSGDYDSKKEPCFREANANKFLPTIYSIIFTLGIVGNGLVILV								62
Dd	7	GIDINIFDONSSTENSGSDFEDEFIECPFMHNSDDFNRIPLTIYSFIFFLLGIIGNGLVVV								66
OY	63	MOYOKRLBMTDKYRLHLVSADLLTVITLPFAVDVANVMYTGNFCLCKAVHYITYYNLKS								122
Dd	67	MOYOKRSRMTDKYRLHLVSADLLVEFVLTPFMSVDAIGMYKEPFLCKAVHYITYYNLS								126
OY	123	SYLIAAFISLDRYLAIVHAATNSQRPRLKLAEGVYGVWIPALLTIPPIFANSEAD								182
Dd	127	SVLIAAFISLDRYLAIVHAATNSQSRKMADKYVAAGWLPALLLTPLVPVAPARSDENG								186
OY	183	RXYCDRFYP--NDLMVVVFPOFHIMVGDLDPGYILSCYCIIISKSLSHSKGHOKRKALK								239
Dd	187	GVCCDRIRYIEKRREIMVTGVRFLHTITVGDILPGILLICVYIISKLSSKHOKRKALK								246
OY	240	TTVIIILIAFFACWLPRYYIGISTDSFLLETKIOGCCEFWNTVKRWISTETALAFFHCCLMP								299
Dd	247	TVIIILIAFFACWLPYYVCLTDTFMELGTGVKGDCIMENTLMAISITETALAFFHCCLMP								306
OY	300	IIXAFLGAFKRKSAAOHALTSVRGSSELKLSGKKRGKGGHSVSTESSSSSFHSS								352
Dd	307	IIXAFLGAFKRKSQAONALFSVRGSSLKLLS-KRAGLSVSSTESSSSSFHSS								358

RESULT	5		
042445			
ID	042445	PRELIMINARY:	PRT: 357 AA.
AC	042445:		
DT	01-JAN-1998 (TREMBLrel. 05, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)		
DE	CXC CHEMOKINE RECEPTOR.		
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;		
OC	Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;		
OC	Salmoniformes; Salmonidae; Oncorhynchus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	DANIELS G.D., CHARLEMAGNE J., SECOMBS C.J.:		
RT	"Cloning and sequencing of a rainbow trout, <i>Oncorhynchus mykiss</i> ,		
RT	chemokine receptor homolog.";		
RL	Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: INTERFERAL MEMBRANE PROTEIN (BY SIMILARITY)		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
DR	EMBL: AJ001039; CAA04493.1; -		
DR	PFAM: PF00001; 7tm.1.1.		
DR	PROSITE: PS00237; G_PROTEIN_RECEPTOR.1.		
DR	G-Protein coupled receptor; Transmembrane; Glycoprotein.		
SQ	SEQUENCE 357 AA: 39817 MW: 608925FE CRG32:		

Query Match	63.4%	Score 1161;	DB 13;	Length 357;
Best Local Similarity	64.5%;	Pred. No. 8e-86;		
Matches 225;	Conservative 50;	Mismatches 64;	Indels 10;	Gaps 7;

[illegible][illegible]

RESULT	6		
093247			
ID	093247	PRELIMINARY;	PRT; 353 AA.
AC	093247;		
DT	01-NOV-1998	(TrEMBLrel. 08, Created)	
DT	01-NOV-1998	(TrEMBLrel. 08, last sequence update)	
DT	01-MAY-1999	(TrEMBLrel. 10, last annotation update)	
DE	CXCR4.		
OS	Cyprinus carpio (Common carp).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;		
OC	Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinoidae; Cyprinidae; Cyprininae; Cyprinus.		

RP SEQUENCE FROM N.A.
RA FUJIKI K., NAKAO M., SHIN D., YANO T.:
RT "cDNA cloning of a carp homologue of mammalian CXCR4":
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases
CC 1. SUBCELLULAR LOCATION: INTERNAL MEMBRANE PROTEIN (By SIMILARITY)
CC 2. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AB012310; EMBL32797.1; --
DR PIRAM: PF00001; 7tm1.1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SEQUENCE 353 AA: 23DD5347 CRC32:
G

Query Match	61.3%	Score 1121.5	DB 13	Length 353
Best Local Similarly	64.1%	Pred. No. 1.2e-82		
Best 223, Conservative	49	Mismatches 67	Indels 9	Gaps 7

Qy	10	DNNEEMSGGYDSKMEKCEPFEEENANKIFLPTIYISIIIFLTGIVGKVIYLVWGQYKXL	63
Dp	10	DN-SDDSSGGFD--FDELCDLTKSNDFOKIFLPVAVYIIFVGLITIGLGVLVWVGFOKKS	67
Qy	70	RSMTDKYRLHLSVADLLFVILPFPMAVDAAVMYFNGFELKAVHVIYTVLYSSVLLIAF	129
Dp	68	KNMDDKYRLHLSIDLLFVILPFPMAVDAAQWFGFELCYVMYITLVNLSVLLIAF	127
Qy	130	ISLDRYLATVHATNSOPRKILAKKVVYVGVWIPALLTTPDFEAVNSEADRYICDRF	189
Dp	128	ISLDRYLAVNATNSQNRFRILAKKVIYLGWLPASLLTVPDLVEAFVHDTGMNTICELT	187
Qy	190	YP---NDLWVVFQFOHIMWGLLPGVILVLSYCIILISKLS-HSKHQ-KRKALKTVIL	244
Dp	188	YPLQGNITWAKVAFEFQHFHIFVGFLLPGVILITCYCIILISKLSKNSGQALRKRAKLTIVIL	247
Qy	245	ILAFACGLPVYIISISDSFLLIIEIQOGFEFNTVHKMISTEFALAFPPCCINPLIYAF	304
Dp	248	ILCFEFCMLPFCACILVDITVLMVAVISHTCFLBQGLKEMIFPFTALVAFPPCCINPLIYAF	307
Qy	305	LGAKFRTISAQHALTVSVRSGSLKTLISGKRGKSHSVSTEESSSFHSS	352
Dp	308	LGVFFSKARNAL--SISRSRSHKMLTK-KRPPISSVSTEESSSVLSS	353

RESULT	7	PRT:	367	AA.
088410				
ID	088410:	PRELIMINARY:		
AC	088410:			
DT	01-NOV-1998	(TREMBLrel . 08.	Created	
DT	01-NOV-1998	(TREMBLrel . 08.	Last sequence update)	
DT	01-MAY-1999	(TREMBLrel . 10.	Last annotation update	
DE	CHEMOKINE RECEPTOR CXCR3.			


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Db 242 HRAIRVIAVVLVLACQIPH-----NMVLTAVNTKRGVSGCTENVLATRVAAVY 295
OY 290 LAFFHCCLNPILYAFAGFKTSAOHALTSVSRGSSKLKLS-----KGRGSHSVST 342
Db 296 LAFFHCCLNPILYAFAGFKT-----RNYFMKIMKDVCMRRKMKMGFICARY 343
OY 343 ESES 346
Db 344 YSES 347

RESULT 10
097571 PRELIMINARY: PRT: 356 AA.
AC 097571:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE INTERLEUKIN-8 RECEPTOR.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN
RP SEQUENCE FROM N.A.
RC STRAIN-BRED BEAGLE;
RA CHANG Y.F., NOVOSSEL V., CHANG C.F.;
RT "The isolation and sequence of canine interleukin-8 receptor
  homolog.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047047; AAC98968.1; -.
KM Receptor.
SQ SEQUENCE 356 AA; 40505 MW; C2B7961F CRC32;

Query Match 30.8%; Score 564; DB 6; Length 356;
Best Local Similarity 35.2%; Pred. No. 6.2e-38;
Matches 128; Conservative 69; Mismatches 129; Indels 38; Gaps 9;

OY 10 DNYTEEMSGDYDSM-----KEPCFREANANKIFLPITYSIIFLTGIVGNG 57
Db 7 DNYTEEDLEFGDIDNTYNTTEMPRIIPADSNPC-RPESLDINKYAVVIVYLVFLNLGNS 65
OY 58 LVILVMGYOKRLRMTDKYRLHLSVADLFLVITLPEFAVDAVANMYGFNLCRAVHIYT 117
Db 66 LVIMVVLVSRVSHSYTDVYLLNLATLADLLFALTLPIWASVKWGFGLPKIVSLNE 125
OY 118 VNLVSSVLIAFISLDRIYAIYHATNSQRPRLAEKVYVGVWIPALLITPDIIFAN- 177
Db 126 VNFYSGIILLASISMDRYLAIVHATRLTQKRHWV-KFICLIGWALSLILSLPIFVFRRA 184
OY 177 VSEADRYICDRFYPNNDLWVVFQFOHIM-----VGLLPGLVILSCCIIISKLSHK 230
Db 185 IMPPISSPYC-----YEDMKTNTTKLIYVRALPQTFGFVPLMIMFCGLTFLTEFNH 240
OY 231 GHOKRAKLTIVILIAFACWLPYIYGISIDSFILLEIKOGCEPENTVHKWISTEAL 290
Db 241 MQOKRAMRVIAVAVLVFLCWLPR-NLVADTLMRLOIMEEQCRNDRIGALDTELL 298
OY 291 AFFHCCCLNPILYAFAGFKT-----KTSOHALTSVSRGSSKLKLSGKRGSHSVSTESE 345
Db 299 GFHSCCLNPILYAFIGOKFRHGLKIMAFHGLI-----SKREYLPDRSRPSEVSGSSANT 352

OY 346 SSSF 349
Db 353 STTF 356

RESULT 11
093281 PRELIMINARY: PRT: 392 AA.
ID 093281:
AC 093281:
DT 01-NOV-1998 (TREMBlrel. 08, Created)

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DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PUTATIVE CHEMOKINE RECEPTOR.
GN CRL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
  Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN
RP SEQUENCE FROM N.A.
RX MEDLINE; 98244380.
RA GUPTA S.K., PILARISETTI K., GRAY S.L., STADEL J.M.;
RT "Molecular cloning of a novel chemokine receptor-like gene from early
  stage chick embryos.";
RL Biochem. Mol. Biol. Int. 44:673-681(1998).
DR EMBL; AF029369; AAC23950.1; -.
DR PFAM; PF00001; 7tm_1; 2.
SQ SEQUENCE 392 AA; 44760 MW; 429466D8 CRC32;

Query Match 29.7%; Score 544; DB 13; Length 392;
Best Local Similarity 32.9%; Pred. No. 2.8e-36;
Matches 118; Conservative 83; Mismatches 130; Indels 28; Gaps 10;

OY 7 YTSNDYTEEMSGDYDSMKKEPCFREAN--AN----FNKIFLPITYSIIFLTGIVGNGLV 59
Db 43 YEANTPTSL-EGYF-----CFNPSSLMANORDPFRKVFIFPLAYILMFGVIGVQNALV 95
OY 60 ILVMGYOKRLRMTDKYRLHLSVADLFLVITLPEFAVDAVANMYGFNLCRAVHIYT 119
Db 96 LVILRFRKSRPTTENFLEHITLAILLTPFPFVSIVSLAGVGTFLKILSAVHKIN 155
OY 120 LVSSVLIAFISLDRIYAIYHATNSQRPRLAEKVYVGVWIPALLITPDIIFAN-S 178
Db 156 FYLHEHAAGLHRVDRIYAIYHATNRARARSIHLTCTAILWSSLLTLPDIIMEYWT 215
OY 179 EADDRYICDRFP-----NDLWVVFQFOHIMVGLIPGIYILSCYCIISKLSHSGH 232
Db 216 DSNRSIC--YRPEGHIGNNNWAT-RFLYHSVGFPMPLVMCYAIWATLQSQRL 272
OY 233 QKRAKLTIVILIAFACWLPYIYGISIDSFILLEIKOGCEPENTVHKWISTEALAF 292
Db 273 QOKAVRAVIAVLTGVFLCWSPIYHIVIFLNTLKEAPAKDCLLDHDLTAIMVTEAIGF 332
OY 299 FHCCCLNPILYAFAGFKTSAOHALTSVSRGSSKLKLSGKRGSHSVSTESSES 347
Db 333 THCCCLNPILYAFAGFKTSAOHALTSVSRGSSKLKLSGKRGSHSVSTESSES 391

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RESULT 12
008707 PRELIMINARY: PRT: 378 AA.
ID 008707:
AC 008707:
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE CHEMOKINE (C-C) RECEPTOR 9 (BETA-CHEMOKINE RECEPTOR D6).
GN CMKBR9
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN
RP SEQUENCE FROM N.A.
RC STRAIN-C3H;
RA NIBBS R.J.B., WYLLIE S.M., PRAGNELL I.B., GRAHAM G.J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12879; CAA73379.1; -.
DR MGI; MGI:1096320; CMKBR9.
DR PFAM; PF00001; 7tm_1; 1.
SQ SEQUENCE 378 AA; 43255 MW; E19F18F5 CRC32;

Query Match 29.3%; Score 535.5; DB 11; Length 378;
Best Local Similarity 30.7%; Pred. No. 1.3e-35;

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RC	STRAIN-SPRAGUE DAWLEY;	
RX	MEDLINE; 98318173.	
RA	JING Y., SALAPANCA M.N., ADHICARI S., XIA Y., FENG L.,	
RA	DELEBIE C.M., PENNELL N.A., STREIT W.J., HARRISON J.K.;	
RT	"Chemokine receptor expression in cultured gila and rat experimental	
RT	allergic encephalomyelitis."	
RL	J. Neuroimmunol. 86:1-12(1998).	
CC	-I- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5	
CC	CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR	
CC	CALCIUM IONS LEVEL (BY SIMILARITY).	
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)	
CC	-I- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND	
CC	MACROPHAGES.	
CC	-I- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC	
CC	ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.	
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR	EMBL; U77349; AAC03242.1; .	
DR	PROSITE: PS00237; G-PROTEIN_RECEPTOR, 1.	
DR	PFAM: Pf00001; 7tm_1.1; 1.	
KW	G-protein coupled receptor; Transmembrane.	
FT	DOMAIN	1 60
FT	TRANSMEM	61 81
FT	DOMAIN	82 91
FT	TRANSMEM	92 112
FT	DOMAIN	113 128
FT	TRANSMEM	129 149
FT	DOMAIN	150 170
FT	TRANSMEM	171 191
FT	DOMAIN	192 220
FT	TRANSMEM	221 241
FT	DOMAIN	242 256
FT	TRANSMEM	257 277
FT	DOMAIN	278 301
FT	TRANSMEM	302 322
FT	DOMAIN	323 373
FT	DISULFID	126 203
EQ	SEQUENCE	373 AA: 42763 MW: 1457808 CRC32:

Query Match	28.5%	Score	521.5	DB	11	Length	373
Best Local Similarity	34.9%	Pred	No. 1.7e-34				
Matches	107	Conservative	67	Mismatches	116	Indels	17
						Gaps	8

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OY 14 EEMSG-----DYOSMKPCFREANENANKLEPLTSLIFLITGNGVILVMGQOK 68
Db 27 QELDGGATTPPYDD-DGRCNKTSYKOGANILPLPSLVITFSGVGMALYIILISCK 85
OY 69 LRSMTDKRLHLSVADLLFVITLTPMAVDAYANMYFGNLFCKAAHVITYNLVSSVTLA 128
Db 86 LKSMIDILFNLAIISDLLELTLTFPMWAIYANENWFGIMCKLTLGTALHIEFGGIEFII 145
OY 129 FISLDRIYAIWATGNSOPRKLAEKVYVGVWVIRALLTLTPDFIPANVSADRYICDR 188
Db 146 LITIDRIYAIWAFALKARIVTGVITSVTWVAVFASIRGLITFKSEDDQDHNSGCR 205
OY 189 FYRPNDLVWVFOFHIM--VGLILPGVILSCYIIISKLSSHKGOKR-KALKTTVIL 244
Db 206 YEPFL-IMK--NFOTIMNIIISLPLRLVMVICYSGIIHTLFCRNEKKRRRAVRLFAI 261
OY 245 ILAFAACALPYIGISIDSLILEI-KOGSEFNVTWAKVISTEALAFKSCNPLPIYA 303
Db 262 MIYVFLFMTPRNYVLFLETF--QELGSLGNSVNDVMHNDQAMQVETLGMTHSCVNPITYA 319
OY 304 FLGAKFK 310
Db 320 FVGGEFR 326

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OM protein - protein search, using sw model

Run on: September 14, 1999, 09:52:22 ; Search time 10.44 Seconds

(without alignments)
953.107 Million cell updates/sec

Title: US-09-104-063-4
Perfect score: 1830
Sequence: 1 MEGISITSDNTTEEMSGD.....KRGHSSVTESSSSFHSS 352

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1830	100.0	352	1 CCR4_HUMAN	P30991 homo sapien
2	1813	99.1	352	1 CCR4_PAPAN	P56491 papio anubi
3	1806	98.7	352	1 CCR4_MACFA	Q28474 macaca fasc
4	1803	98.5	352	1 CCR4_MACMU	P79334 macaca mula
5	1795	98.1	352	1 CCR4_CERTO	O62147 cercocebus
6	1741.5	95.2	353	1 CCR4_FELCA	P56498 felis silve
7	1722.5	94.1	353	1 CCR4_BOVIN	P25930 bos taurus
8	1678.5	91.7	359	1 CCR4_MOUSE	P70658 mus musculu
9	1673	91.4	349	1 CCR4_RAT	O08565 rattus norv
10	934.5	51.1	192	1 CCR4_SHEEP	Q28553 ovis aries
11	600.5	32.8	360	1 CCR4_HUMAN	P51679 homo sapien
12	581.5	31.8	359	1 IL8B_RAT	P35407 rattus norv
13	576.5	31.5	368	1 CCR3_HUMAN	P49682 homo sapien
14	568	31.0	360	1 IL8B_HUMAN	P25025 homo sapien
15	567	31.0	353	1 IL8B_MACMU	Q28519 macaca mula
16	566.5	31.0	353	1 IL8B_GORGO	Q28422 gorilla gor
17	566	30.9	353	1 IL8B_PANTR	Q28807 pan troglod
18	564.5	30.8	360	1 CCR4_MOUSE	P51680 mus musculu
19	564	30.8	355	1 IL8A_RABIT	P21109 oryctolagus
20	563.5	30.8	350	1 IL8A_GORGO	P55919 gorilla gor
21	563.5	30.8	350	1 IL8A_PANTR	P55920 pan troglod
22	563	30.8	378	1 CCR7_MOUSE	P47774 mus musculu
23	558	30.5	358	1 IL8B_RABIT	P35344 oryctolagus
24	557.5	30.5	357	1 GC96_HUMAN	P51686 homo sapien
25	557.5	30.5	350	1 IL8A_HUMAN	P25024 homo sapien
26	557	30.4	378	1 CCR7_HUMAN	P32248 homo sapien
27	549.5	30.0	355	1 GPRD_HUMAN	P49338 homo sapien
28	540	29.5	372	1 BLR1_HUMAN	P32302 homo sapien
29	539	29.5	359	1 IL8B_MOUSE	P33403 mus musculu
30	536	29.2	374	1 BLR1_MOUSE	P33402 mus musculu
31	533.5	29.2	374	1 CCR6_HUMAN	P51684 homo sapien
32	533.5	29.2	353	1 CCR6_MOUSE	P56484 mus musculu
33	529	28.9	374	1 BLR1_RAT	P34997 rattus norv
34	528	28.9	374	1 CCR2_HUMAN	P41597 homo sapien
35	527	28.8	342	1 BONT_CERRA	O18883 cercopithec
36	527	28.8	355	1 CCR8_HUMAN	P51685 homo sapien
37	525.5	28.7	342	1 BONT_MACNE	O19024 macaca neme
38	524.5	28.7	342	1 BONT_HUMAN	O00574 homo sapien
39	523	28.5	360	1 IL8B_BOVIN	Q28003 bos taurus
40	521.5	28.4	349	1 IL8A_RAT	P70612 rattus norv
41	519.5	28.4	373	1 CCR2_MOUSE	P51683 mus musculu
42	516	28.2	352	1 CCR5_MOUSE	P56493 ceropithec
43	514.5	28.1	354	1 GPRD_RAT	P35411 rattus norv

ALIGNMENTS

44	512	28.0	352	1 CCR5_PANTR	P56440 pan troglod
45	509	27.8	352	1 CCR5_GORGO	P56439 gorilla gor
RESULT 1					
CCR4_HUMAN					
ID CCR4_HUMAN	STANDARD;	PRT;	352 AA.		
AC P30991; P56438;					
DT 01-JUL-1993 (REL. 26, CREATED)					
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)					
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)					
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)					
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED					
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCR1) (FB22) (NPYRL)					
DE (HM89).					
GN CXCR4.					
OS HOMO SAPIENS (HUMAN), AND PAN TROGLODYTES (CHIMPANZEE).					
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;					
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.					
RN [1]					
RP SEQUENCE FROM N.A.					
RC SPECIES-HUMAN; TISSUE=LUNG;					
RX MEDLINE; 93319629.					
RA HERZOG H., HORT Y.J., SHINE J., SELBIE L.A.;					
RT "Molecular cloning, characterization, and localization of the human					
RT homolog to the reported bovine NPY Y3 receptor: lack of NPY binding					
RT and activation."					
RL DNA CELL BIOL. 12:465-471(1993).					
RN [2]					
RP SEQUENCE FROM N.A.					
RC SPECIES-HUMAN; TISSUE=BRAIN;					
RX MEDLINE; 94052833.					
RA JAZIN E.E., YOO H., BLOMOVIST G., YEE F., WENG G., WALKER M.W.,					
RA SALON J., LARHAMAR D., WAHLESTEDT C.R.;					
RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its					
RT human homologue, confers neither NPY binding sites nor NPY					
RT responsiveness on transfected cells."					
RL REGUL. PEPT. 47:247-258(1993).					
RN [3]					
RP SEQUENCE FROM N.A.					
RC SPECIES-HUMAN; TISSUE=SPLEEN;					
RX MEDLINE; 93315164.					
RA FEDERSPIEL B., DELANEY A.D., CLARK-LEWIS I., JIRIK F., DUNCAN A.M.,					
RA SCHAPPERT K.T., MELHADO I.;					
RT "Molecular cloning of the cDNA and chromosomal localization of the					
RT gene for a putative seven-transmembrane segment (7-TMS) receptor					
RT isolated from human spleen."					
RL GENOMICS 16:707-712(1993).					
RN [4]					
RP SEQUENCE FROM N.A.					
RC SPECIES-HUMAN; TISSUE=LEUKOCYTE;					
RX MEDLINE; 94103215.					
RA LOESCHER M., GEISER T., O'REILLY T., ZWAHLEN R., BAGGIOLINI M.,					
RA MOSER B.;					
RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that					
RT is highly expressed in leukocytes."					
RL J. BIOL. CHEM. 269:232-237(1994).					
RN [5]					
RP SEQUENCE FROM N.A.					
RC SPECIES-HUMAN; TISSUE=MONOCYTES;					
RX MEDLINE; 94092629.					
RA NOMURA H., NIELSEN B.W., MATSUSHIMA K.;					
RT "Molecular cloning of cDNAs encoding a ID78 receptor and putative					
RT leukocyte chemotactic peptide receptors."					
RL INT. IMMUNOL. 5:1239-1249(1993).					
RN [6]					
RP SEQUENCE FROM N.A.					
RC SPECIES-HUMAN;					
RA WEGNER S.A., EHRENBERG P.K., CHANG G., DAYHOFF D.E., MICHAEL N.L.;					
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.					

Query	Match	Best Local Similarity	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
QY	1	MEGISITSDNYTEHMSGSDYDSKKECFRENNANKILPLTIYSITFLTGIVNGLVI	100.0%;	DB 1;	352;	352	0	0	0	0
Db	1	MEGISITSDNYTEHMSGSDYDSKKECFRENNANKILPLTIYSITFLTGIVNGLVI	100.0%;	DB 1;	352;	352	0	0	0	0
QY	61	LYMVGQKRLKSMDEKYLHLHVSADLLFVITLPEFAVDVAVNWFNGNLCRAVHYTYVNL	100.0%;	DB 1;	352;	352	0	0	0	0
Db	61	LYMVGQKRLKSMDEKYLHLHVSADLLFVITLPEFAVDVAVNWFNGNLCRAVHYTYVNL	100.0%;	DB 1;	352;	352	0	0	0	0
QY	121	YSSVLLIAFLSLDRYLAIVATNSQREPKLLAEKVYVGVWIPALLTIPDFIFANYSEA	100.0%;	DB 1;	352;	352	0	0	0	0
Db	121	YSSVLLIAFLSLDRYLAIVATNSQREPKLLAEKVYVGVWIPALLTIPDFIFANYSEA	100.0%;	DB 1;	352;	352	0	0	0	0
QY	181	DDRITCDREFPNDLMMVYFQFOHIMGGLIPGIVTILSCYCLIIISKSHSGHOKRAKLT	100.0%;	DB 1;	352;	352	0	0	0	0
Db	181	DDRITCDREFPNDLMMVYFQFOHIMGGLIPGIVTILSCYCLIIISKSHSGHOKRAKLT	100.0%;	DB 1;	352;	352	0	0	0	0
QY	241	TVILIIAFAFCWLPYYIGISIDSIFLLEIIKQCEPENTYHKMISTEALAFHCCINPI	100.0%;	DB 1;	352;	352	0	0	0	0
Db	241	TVILIIAFAFCWLPYYIGISIDSIFLLEIIKQCEPENTYHKMISTEALAFHCCINPI	100.0%;	DB 1;	352;	352	0	0	0	0
QY	301	LYAFLEAKKETSQHALTSYRSRSSLKILSKGRGGSHSVSTSESSSFHSS	100.0%;	DB 1;	352;	352	0	0	0	0
Db	301	LYAFLEAKKETSQHALTSYRSRSSLKILSKGRGGSHSVSTSESSSFHSS	100.0%;	DB 1;	352;	352	0	0	0	0

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 CC or send an email to license@isb-sib.ch).

DR EMBL: AF031089; G2625094; -
 DR GCRDB: GCR_2512; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT TRANSMEM 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT TRANSMEM 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT TRANSMEM 221 240
 FT TRANSMEM 241 261
 FT TRANSMEM 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT CARBOHYD 11 11
 FT DISULFID 109 186
 SQ SEQUENCE 352 AA; 39751 MW; 273DB8EE CRC32;

Query Match 99.1%; Score 1813; DB 1; Length 352;
 Best Local Similarity 98.9%; Pred. No. 2.6e-116;
 Matches 348; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITYSDNTYEMSGSDYDMSKEPCFEENANFNKIFLPITYSIIFLTGIVNGLYI 60
 DB 1 MEGISITYSDNTYEMSGSDYDMSKEPCFEENANFNKIFLPITYSIIFLTGIVNGLYI 60
 QY 61 LVNGYOKKLRSMYDKYRLHLSVADLLFVITLPPWAVDAVANMFGNFKCAVHYITVNL 120
 DB 61 LVNGYOKKLRSMYDKYRLHLSVADLLFVITLPPWAVDAVANMFGNFKCAVHYITVNL 120
 QY 121 YSSVLLAFISDRYLAIVHATNSORPKRLAEKVYVGWIPALLITPDIFFAVNSEA 180
 DB 121 YSSVLLAFISDRYLAIVHATNSORPKRLAEKVYVGWIPALLITPDIFFAVNSEA 180
 QY 181 DRYICDREYPNDLVWVVEFOFHIMVGLIPGIVILSCYCIISKLSHSGHQRKRLAKT 240
 DB 181 DRYICDREYPNDLVWVVEFOFHIMVGLIPGIVILSCYCIISKLSHSGHQRKRLAKT 240
 QY 241 TVLLILAFACWLPYYIGISIDSFILLEITIKOCCEFEENVHAKWISTEALAFHCLNPI 300
 DB 241 TVLLILAFACWLPYYIGISIDSFILLEITIKOCCEFEENVHAKWISTEALAFHCLNPI 300
 QY 301 LYAFILAKFKTSQAHALTSVSRGSSSLKLSKRGKRGHSSVTESSSSPHSS 352
 DB 301 LYAFILAKFKTSQAHALTSVSRGSSSLKLSKRGKRGHSSVTESSSSPHSS 352

RESULT 3
 CCR4_MACFA STANDARD; PRT: 352 AA.
 ID CCR4_MACFA 028474;
 AC 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 GN (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (LESTR).
 OS MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLUS MONKEY).
 GN EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA;

OC PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TATSUMI M., TAKAHASHI H.;
 RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).

DR EMBL: D86579; G1468949; -
 DR GCRDB: GCR_1143; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 KW PFAM: PF00001; 7tm_1; 1.
 FT G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT TRANSMEM 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT TRANSMEM 133 154
 FT TRANSMEM 155 175
 FT TRANSMEM 176 200
 FT TRANSMEM 201 220
 FT TRANSMEM 221 240
 FT TRANSMEM 241 261
 FT TRANSMEM 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT CARBOHYD 11 11
 FT DISULFID 109 186
 SQ SEQUENCE 352 AA; 39753 MW; 7EDA93BA CRC32;

Query Match 98.7%; Score 1805; DB 1; Length 352;
 Best Local Similarity 98.3%; Pred. No. 7.6e-116;
 Matches 346; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEGISITYSDNTYEMSGSDYDMSKEPCFEENANFNKIFLPITYSIIFLTGIVNGLYI 60
 DB 1 MEGISITYSDNTYEMSGSDYDMSKEPCFEENANFNKIFLPITYSIIFLTGIVNGLYI 60
 QY 61 LVNGYOKKLRSMYDKYRLHLSVADLLFVITLPPWAVDAVANMFGNFKCAVHYITVNL 120
 DB 61 LVNGYOKKLRSMYDKYRLHLSVADLLFVITLPPWAVDAVANMFGNFKCAVHYITVNL 120
 QY 121 YSSVLLAFISDRYLAIVHATNSORPKRLAEKVYVGWIPALLITPDIFFAVNSEA 180
 DB 121 YSSVLLAFISDRYLAIVHATNSORPKRLAEKVYVGWIPALLITPDIFFAVNSEA 180
 QY 181 DRYICDREYPNDLVWVVEFOFHIMVGLIPGIVILSCYCIISKLSHSGHQRKRLAKT 240
 DB 181 DRYICDREYPNDLVWVVEFOFHIMVGLIPGIVILSCYCIISKLSHSGHQRKRLAKT 240
 QY 241 TVLLILAFACWLPYYIGISIDSFILLEITIKOCCEFEENVHAKWISTEALAFHCLNPI 300
 DB 241 TVLLILAFACWLPYYIGISIDSFILLEITIKOCCEFEENVHAKWISTEALAFHCLNPI 300
 QY 301 LYAFILAKFKTSQAHALTSVSRGSSSLKLSKRGKRGHSSVTESSSSPHSS 352
 DB 301 LYAFILAKFKTSQAHALTSVSRGSSSLKLSKRGKRGHSSVTESSSSPHSS 352

RESULT 4

CCR4_MACMU STANDARD; PRT; 352 AA.

AC P79394; 002745; 046428;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS MACACA MULATTA (RHEBUS MACAQUE).
 OC EURAYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-INDIAN MACAQUE;
 RX MEDLINE: 97213934.
 RA CHEN Z., ZHOU P., HO D.D., LANDAU N.R., MARX P.A.;
 RT "Genetically divergent strains of simian immunodeficiency virus use CCR5 as a coreceptor for entry.";
 RL J. VIROL. 71:2705-2714(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97268687.
 RA EDINGER A.L., AMEDEE A., MILLER K., DORANZ B.J., ENDRES M.,
 RA SHARRON M., SAMSON M., LU Z.-H., CLEMENTS J.E., MURPHEY-CORB M.,
 RA PIPPER S.C., PARMENTIER M., BRODER C.C., DOMS R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 94:4005-4010(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CHINESE;
 RX MEDLINE: 98252393.
 RA PRETET J.-L., GUILLET J.-G., BUTOR C.;
 RT "New widespread CXCR4 allele in rhesus macaques does not predict subspecies or clinical evolution.";
 RL AIDS RES. HUM. RETROVIRUSES 14:639-641(1998).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: U73740; G1899056; -
 DR EMBL: U93311; G1934671; -
 DR EMBL: AF001928; G2911294; -
 DR GCRDB: GCR.1297; -
 DR GCRDB: GCR.1640; -
 DR PROSITE: PS00237; G.PROTEIN_RECEPTOR; 1.
 DR PRAM: PF00001; 7tm.1; 1.
 KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352

FT CARBOHYD 11 11 POTENTIAL.
 FT DISULFID 109 186 BY SIMILARITY.
 FT CONFLICT 67 67 K -> E (IN REF. 2).
 FT CONFLICT 214 214 D -> V (IN REF. 2 AND 3).
 FT CONFLICT 348 348 S -> N (IN REF. 2).
 SQ SEQUENCE 352 AA; 39739 MW; 3C3344BB CRC32;

Query Match 98.5%; Score 1803; DB 1; Length 352;
 Best Local Similarity 98.3%; Pred. No. 1, 2e-115;
 Matches 346; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEGISITSDNTYEEMSGSDYDSMKPECFREANANKIFLPITYSIIFLTGVNGLYI 60
 DB 1 MEGISITSDNTYEEMSGSDYDSMKPECFREANANKIFLPITYSIIFLTGVNGLYI 60
 QY 61 LVNGYOKRLKSMYDKYRLHLSVADLLFVITLPPMAVDAAVMYFGLCKAVHVIYTVL 120
 DB 61 LVNGYOKRLKSMYDKYRLHLSVADLLFVITLPPMAVDAAVMYFGLCKAVHVIYTVL 120
 QY 121 YSSVLIAFISLDRIYAIYHATNSQRPRLAKRYVYGVWIPALLITPDLFANVSA 180
 DB 121 YSSVLIAFISLDRIYAIYHATNSQRPRLAKRYVYGVWIPALLITPDLFANVSA 180
 QY 181 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVISCYCIITSLKSHKGRKALKT 240
 DB 181 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVISCYCIITSLKSHKGRKALKT 240
 QY 241 TVIILIAFACWLPYYIGISIDSFILLEITIKOCFENYVHKWISTEALAFHCLNPI 300
 DB 241 TVIILIAFACWLPYYIGISIDSFILLEITIKOCFENYVHKWISTEALAFHCLNPI 300
 QY 301 LVAFLEAKFTSQHALLTSRSKSLIKSKGRGSHSVSTSESSFSHS 352
 DB 301 LVAFLEAKFTSQHALLTSRSKSLIKSKGRGSHSVSTSESSFSHS 352

RESULT 5
 CCR4_CERTO STANDARD; PRT; 352 AA.

AC 062747;
 DT 15-DEC-1998 (REL. 37, CREATED)
 DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS CERCOCERUS TORQUATUS ATYS (RED-CROWNED MANGABEY) (SOOTY MANGABEY).
 OC EURAYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; CERCOCERUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98321155.
 RA CHEN Z., GETTIE A., HO D.D., MARX P.A.;
 RT "Primary siyem isolates use the CCR5 coreceptor from sooty mangabeys naturally infected in west Africa: a comparison of coreceptor usage of primary siyem, HIV-2 and siyemac.";
 RL VIROLOGY 246:113-124(1998).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: AF051906; G3135304; -
 DR PROSITE: PS00237; G.PROTEIN_RECEPTOR; 1.

KM G-PROTEIN COUPLED RECEPTOR: TRANSMEMBRANE: GLYCOPROTEIN.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 113 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT TRANSMEM 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT CAROXYD 11
 FT DISULFID 109
 SQ SEQUENCE 352 AA: 39648 MW: 88464DAD CRC32:
 BY SIMILARITY.

Query Match 98.1%; Score 1795; DB 1; Length 352;
 Best Local Similarity 97.7%; Pred. No. 4.2e-115;
 Matches 344; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

OY 1 MEGISITYSDNTEEMSGSDYDMSKPCFRENNANPKIFLPTIYSITFLTGIVGNGLY 60
 DB 1 MEGISITYSDNTEEMSGSDYDMSKPCFRENNANPKIFLPTIYSITFLTGIVGNGLY 60
 OY 61 LVMGYQKRLSRMTDKYRHLVSADLLFVITLPEFAVDAVANNYFGNFKCAVHIVTVNL 120
 DB 61 LVMGYQKRLSRMTDKYRHLVSADLLFVITLPEFAVDAVANNYFGNFKCAVHIVTVNL 120
 OY 121 YSSVLLAFISLDRLAIYVHATNSQRPRLAEKYYVGVWIPALLITPDIFANVSA 180
 DB 121 YSSVLLAFISLDRLAIYVHATNSQRPRLAEKYYVGVWIPALLITPDIFANVSA 180
 OY 181 DDRYICDRFPNDLWVVFQFQIHWGLILPGIVILSCYCIISKLSHSGHOKRKALKT 240
 DB 181 DDRYICDRFPNDLWVVFQFQIHWGLILPGIVILSCYCIISKLSHSGHOKRKALKT 240
 OY 241 TVIILAFACWLPYYIGISIDSIFLLEIKOGCEFEVTHKWSITELAFHCCLNPI 300
 DB 241 TVIILAFACWLPYYIGISIDSIFLLEIKOGCEFEVTHKWSITELAFHCCLNPI 300
 OY 301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGRGHSSTSESSSFHSS 352
 DB 301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGRGHSSTSESSSFHSS 352

RESULT 6
 CCR4_FELCA STANDARD: PRT: 353 AA.
 AC P36498; P79172; 002700;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS FELIS SILVESTRIS CATUS (CAT).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC CARNIVORA: FISSIPEDIA: FELIDAE: FELIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97404646.
 RA WILDETT B.J., PICARD L., HOSIE M.J., TURNER J.D., ADEKA K.,
 RA CLAPHAM P.R.;
 RT "Shared usage of the chemokine receptor CXCR4 by the feline and human
 RT immunodeficiency viruses.";
 RL J. VIROL. 71:6407-6415(1997).
 RN [2]
 RP SEQUENCE FROM N.A.

RA WILDETT B.J.;
 RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA LERNER D.L., ELDER J.H.;
 RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: U63558; G1842247; -;
 DR EMBL: U92795; G1935045; -;
 DR GCRDB; GCR_1113; -;
 DR GCRDB; GCR_1114; -;
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR: 1.
 KM G-PROTEIN COUPLED RECEPTOR: TRANSMEMBRANE: GLYCOPROTEIN.
 FT DOMAIN 1 40
 FT TRANSMEM 41 64
 FT DOMAIN 65 80
 FT TRANSMEM 81 100
 FT DOMAIN 101 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 155
 FT TRANSMEM 156 176
 FT DOMAIN 177 201
 FT TRANSMEM 202 221
 FT DOMAIN 222 241
 FT TRANSMEM 242 262
 FT DOMAIN 263 286
 FT TRANSMEM 287 306
 FT DOMAIN 307 353
 FT CAROXYD 11
 FT DISULFID 110
 FT CONFLICT 67
 FT CONFLICT 263
 SQ SEQUENCE 353 AA: 39935 MW: 5829DDIE CRC32:
 BY SIMILARITY.
 O -> H (IN REF. 3).
 D -> E (IN REF. 3).

Query Match 95.2%; Score 1741.5; DB 1; Length 353;
 Best Local Similarity 94.6%; Pred. No. 1.8e-111;
 Matches 334; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

OY 1 MEGISITYSDNTE-EMSGSDYDMSKPCFRENNANPKIFLPTIYSITFLTGIVGNGLY 59
 DB 1 MEGISITYSDNTE-EMSGSDYDMSKPCFRENNANPKIFLPTIYSITFLTGIVGNGLY 60
 OY 60 IIVMGYQKRLSRMTDKYRHLVSADLLFVITLPEFAVDAVANNYFGNFKCAVHIVTVN 119
 DB 60 IIVMGYQKRLSRMTDKYRHLVSADLLFVITLPEFAVDAVANNYFGNFKCAVHIVTVN 120
 OY 120 IYSSVLLAFISLDRLAIYVHATNSQRPRLAEKYYVGVWIPALLITPDIFANVSE 179
 DB 120 IYSSVLLAFISLDRLAIYVHATNSQRPRLAEKYYVGVWIPALLITPDIFANVSE 180
 OY 180 ADDRICYDRFPNDLWVVFQFQIHWGLILPGIVILSCYCIISKLSHSGHOKRKALK 239
 DB 180 ADDRICYDRFPNDLWVVFQFQIHWGLILPGIVILSCYCIISKLSHSGHOKRKALK 240
 OY 240 TVIILAFACWLPYYIGISIDSIFLLEIKOGCEFEVTHKWSITELAFHCCLNPI 299
 DB 240 TVIILAFACWLPYYIGISIDSIFLLEIKOGCEFEVTHKWSITELAFHCCLNPI 300
 OY 300 ILYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGRGHSSTSESSSFHSS 352
 DB 300 ILYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGRGHSSTSESSSFHSS 352

DB 301 ILYAFGAKFKTSQAHALTSVSRGSSSLKILSKGRGSHSVSTESSFSHSS 353

RESULT 7

CCRA_BOVIN STANDARD; PRT; 353 AA.

AC P25930;

AD 01-MAY-1992 (REL. 22, CREATED)

DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)

DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCR1).

GN CXCR4.

OS BOS TAURUS (BOVINE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE-LOCUS COERULEUS;

RL MEDLINE: 92100053.

RA RIMLAND J., XIN W., SWEETNAM P., SALJOH K., NESTLER E.J., DUMAN R.S.;

RT "Sequence and expression of a neuropeptide Y receptor cDNA.";

RL MOL. PHARMACOL. 40:869-875(1991).

RN (2)

RP SHOWS THAT IT IS NOT A NPY3-R.

RL MEDLINE: 94052833.

RA JAZIN E.E., YOO H., BLONOVIST G., YEE F., WENG G., WALKER M.W.,

RA SALON J., LARHAMMAR D., WAHLESTEDT C.R.;

RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homologue, confers neither NPY binding sites nor NPY responsiveness on transfected cells.";

RL REGUL. PEPT. 47:247-258(1993).

CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: BRAIN, HEART, KIDNEY, LONG AND LIVER.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE Y, TYPE 3 (NPY3-R).

CC -----

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CC -----

CC EMBL: M86739; -; NOT_ANNOTATED_CDS.

DR PIR: S28787; S28787.

DR GCRDB: GCR_0180; -;

DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.

DR PFAM: PF00001; 7tm_1.1.

KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.

FT DOMAIN 1 40

FT TRANSMEM 41 64

FT DOMAIN 65 80

FT TRANSMEM 81 100

FT DOMAIN 101 111

FT TRANSMEM 112 133

FT DOMAIN 134 155

FT TRANSMEM 156 176

FT DOMAIN 177 201

FT TRANSMEM 202 221

FT DOMAIN 222 241

FT TRANSMEM 242 262

FT DOMAIN 263 286

FT TRANSMEM 287 306

FT DOMAIN 307 353

FT CARBOHYD 11

FT DISULFID 110 187

SQ SEQUENCE 353 AA; 39938 MW; 03DBF100 CRC32;

Query Match 94.1%; Score 1722.5; DB 1; Length 353;

Best Local Similarity 92.4%; Pred. No. 3.4e-110;

Matches 326; Conservative 20; Mismatches 6; Indels 1; Gaps 1;

QY 1 MEGISYTSNDNTE-EMGGADYDSMKPECFREBNANFKIPFTIYSIFLGIYNGV 59

DB 1 MEDIRLFISDNTIEDDGGDDSDMSKPECFREBNANFKIPFTIYSIFLGIYNGV 60

QY 60 IIVMGYQKLRSMTDKRYRLSLVADLFTVITLPEMAVDANVMYEGNLCRAVHYTVN 119

DB 61 IIVMGYQKLRSMTDKRYRLSLVADLFTVITLPEMAVDANVMYEGNLCRAVHYTVN 120

QY 120 LYSVYLILAFISIDRLAIVHATNSRPRKLLAEKVYGVWIPALLTIPDFIANSE 179

DB 121 LYSVYLILAFISIDRLAIVHATNSRPRKLLAEKVYGVWIPALLTIPDFIANSE 180

QY 180 ADDRICYDRFPNDLWVVFVFOHIMWGLDPGIVILSCYCIITISKLSHGOKRAIK 239

DB 181 VDERYICDRFPYSDMLWVVFVFOHIMWGLDPGIVILSCYCIITISKLSHGOKRAIK 240

QY 240 TVVILLIAEFACMLPYIIGISIDSFILBIRKOGCEFFENTVHKWISITELAFHCCCLNP 299

DB 241 TVVILLIAEFACMLPYIIGISIDSFILBIRKOGCEFFENTVHKWISITELAFHCCCLNP 300

QY 300 ILYAFGAKFKTSQAHALTSVSRGSSSLKILSKGRGSHSVSTESSFSHSS 352

DB 301 ILYAFGAKFKTSQAHALTSVSRGSSSLKILSKGRGSHSVSTESSFSHSS 353

RESULT 8

CCRA_MOUSE STANDARD; PRT; 359 AA.

AC P70658; P70346; 009062; 009059; P70233;

DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)

DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).

GN CXCR4 OR LESTR OR CMKAR4 OR SDF1R.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6 X CBA; TISSUE=THYMUS;

RA MOEPPS B., FRODL R., KESSLER H., GIERSCHEK P.;

RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

RN (2)

RP SEQUENCE FROM N.A.

RC STRAIN=129/SV;

RA HEESSEN M., BERMAN M.A., GERARD C., DORF M.E.;

RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

RN (3)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA MEDLINE: 9711334.

RA HEESSEN M., BERMAN M.A., BENSON J.D., GERARD C., DORF M.E.;

RT "Cloning of the mouse fusin gene, homologue to a human HIV-1 co-factor.";

RL J. IMMUNOL. 157:5455-5460(1996).

RN (4)

RP SEQUENCE FROM N.A.

RC TISSUE=BONE MARROW;

RA MEDLINE: 97121456.

RA NAGASAWA T., NAKAJIMA T., TACHIBANA K., IIZASA H., BLEUL C.C.,

RA YOSHIE O., MATSUSHIMA K., YOSHIDA N., SPRINGER T.A., KISHIMOTO T.;

RT "Molecular cloning and characterization of a murine pre-B-cell growth-stimulating factor/stromal cell-derived factor 1 receptor, a murine homolog of the human immunodeficiency virus 1 entry coreceptor fusin.";

```

RL PROC. NATL. ACAD. SCI. U.S.A. 93:14726-14729(1996).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=57BL/6; TISSUE=THYMUS;
RA SUZUKI G., NAKATA Y., UZAMA A., SHIRASAWA T., SAITO T., MITA K.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=THYMUS;
RA SCHUBEL A., BURGSTALLER R., LIPP M.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; X99581; E281127; -
DR EMBL; X99582; E281126; -
DR EMBL; U59760; G1527135; -
DR EMBL; U65580; G1731651; -
DR EMBL; D87747; G1772446; -
DR EMBL; AB000803; G1816446; -
DR EMBL; 280112; E266602; -
DR GCRDB; GCR_1138; -
DR GCRDB; GCR_1387; -
DR GCRDB; GCR_1646; -
DR GCRDB; GCR_1730; -
DR GCRDB; GCR_2592; -
DR MGI; 109563; CMKAR4.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 1 41
FT TRANSMEM 42 65
FT DOMAIN 66 81
FT TRANSMEM 82 101
FT DOMAIN 102 112
FT TRANSMEM 113 134
FT DOMAIN 135 156
FT TRANSMEM 157 177
FT DOMAIN 178 207
FT TRANSMEM 208 227
FT DOMAIN 228 247
FT TRANSMEM 248 268
FT DOMAIN 269 292
FT TRANSMEM 293 312
FT DOMAIN 313 359
FT DISULFID 111 193
FT CARBOHYD 13 13
FT CONFLICT 6 7
FT CONFLICT 216 216
FT SEQUENCE 359 AA; 40426 MW; 1037BAD3 CRC32;

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Query Match 91.7%; Score 1678.5; DB 1; Length 359;
 Best Local Similarity 90.1%; Pred. No. 3.3e-107;
 Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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OY 4 ISIVSDNTTEEMSGDYDSMKEPCFREANFNKIFPTIYSIIFLTGIVNGIIVLM 63
DB 6 VSIYSDNTESEVSGDYDSMKEPCFREANFNKIFPTIYSIIFLTGIVNGIIVLM 65
OY 64 GYOKLRSTMDKRYRLHLSTADLLFVITLFPFAVDAMNMFNGFLCKAVHYITVNLVSS 123

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DB 66 GYOKLRSTMDKRYRLHLSTADLLFVITLFPFAVDAMNMFNGFLCKAVHYITVNLVSS 125
OY 124 VLLAFISIDRYLAIYHAATNSQPRKRLAEKYVYGVWIPALLITPDPFANV-----S 178
DB 126 VLLAFISIDRYLAIYHAATNSQPRKRLAEKYVYGVWIPALLITPDPFADVSGDLS 185
OY 179 EADDRICRFPNDLVVYVFOFQHIMVGLLPGIYILSCYCIILSKLSHGKQRKAL 238
DB 186 GQDRIYICRLYDPSLMMVYVFOFQHIMVGLLPGIYILSCYCIILSKLSHGKQRKAL 245
OY 239 KTVVILILAFPCWLPYVIGISIDSFILLETIKOGCFENTYHKWISTEALAFPHCCLN 298
DB 246 KITVILILAFPCWLPYVIGISIDSFILGVIKOGCFESIYHKWISTEALAFPHCCLN 305
OY 299 PILVAFGLAKFKTSQAHALTVSRGSSILSKRGKSHSVSTESSSFHSS 352
DB 306 PILVAFGLAKFKSSAQHALLNSMRGSSILSKRGKSHSVSTESSSFHSS 359
RESULT 9
ID CCR4_RAT STANDARD: PRI: 349 AA.
CCR4_RAT 008565;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).
GN CXCR4 OR CMKAR4.
OS RATUUS NOREGETICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; RATIUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=SPLEEN;
RA HARRISON J.K., SALAFRANCA M.N.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U90610; G190613; -
DR GCRDB; GCR_1401; -
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 1 36
FT TRANSMEM 37 60
FT DOMAIN 61 76
FT TRANSMEM 77 96
FT DOMAIN 97 107
FT TRANSMEM 108 129
FT DOMAIN 130 151
FT TRANSMEM 152 172
FT DOMAIN 173 197
FT TRANSMEM 198 217
FT DOMAIN 218 237
FT TRANSMEM 238 258
FT DOMAIN 259 282
FT TRANSMEM 283 302
FT DOMAIN 303 349
FT DISULFID 106 183
FT CARBOHYD 8 8

```


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DR EMBL; X85740; G971452; -
DR GCRDB; GCR 2115; -
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFM; PFM0001; 7tm.1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 1 39
FT TRANSMEM 40 67
FT DOMAIN 68 77
FT TRANSMEM 78 98
FT DOMAIN 99 111
FT TRANSMEM 112 133
FT DOMAIN 134 150
FT TRANSMEM 151 175
FT DOMAIN 176 206
FT TRANSMEM 207 226
FT DOMAIN 227 242
FT TRANSMEM 243 267
FT DOMAIN 268 284
FT TRANSMEM 285 308
FT DOMAIN 309 360
FT CARBOHYD 183 183
FT CARBOHYD 194 194
FT DISULFID 110 187
SQ SEQUENCE 360 AA; 41402 MW; 8738E75E CRC32;

Query Match 32.8%; Score 600.5; DB 1; Length 360;
Best Local Similarity 39.7%; Pred. No. 3.1e-34;
Matches 116; Conservative 60; Mismatches 113; Indels 3; Gaps 2;

QY 21 YDSKKEPCFRENANFNKIFLPTISITIFLGIYNGVLIVMGOKLRSTDKRYRL 80
DB 22 YESIPKPTKGIAFGELFLPPLISLVFVGLGNSVYLVLFYKKLRSTDVYLLNL 81
QY 81 SVADLLEVTPEFMAVDVAVMVEFGLCKAVHYVTNLSSVLLAFISDRYLAIVH 140
DB 82 AISDLLEFSLPFGMYADQVVGGLGCKMISMVLYGVFSIGIFVWLMISDRYLAIVH 141
QY 141 ATNSQRPKLLAEKVYVGVWIPALLTIPDFIFANVSEADRYICDRFPY--NDLWVYV 198
DB 142 AVFSLRATLTLYGYITSLATWSAVFASLPGLFSTCYTERNHTYCKTKYSINSTMKVL 201
QY 199 FQFQHIWGLLPGLVILSCYCIISKLSHGKRGKRAKATYVLLILAFACWLPYIIG 258
DB 202 SLENTNIGLVIPGIMFCYSMTIRTLQHKNEKKNKNAFVAVVLFGLFWTPYIV 261
QY 259 ISIDSFILLEIKOGCEPENTVHKWISITELAFPHCLNPLVLAFAKPK 310
DB 262 LLEFLVELVL-QDCPFERLDVAIQATETLAFHCCLNLIYFFLGEKPK 312

RESULT 12
IL8B_RAT STANDARD: PRT: 359 AA.
AC P35407;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR).
GN IL8RB OR CXCR2.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MORIDAE; MURINAE; RATTUS.

RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGE-DAMELEY; TISSUE-LUNG;
RA GOEL A.E., WANG S., ZHOU Y., OEBERG K.;
RL SUBMITTED (FEB-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RM [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-LIVER;
RA KONISHI K., SHIBATA F., MATANABE K., TSURUFUJI S., NAKAGAWA H.,
RA FUJIOKA M.;
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RM [3]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-SPLEEN, AND LUNG;
RX MEDLINE; 97115810.
RA DUNSTAN C.-A.N., SALAFRANCA M.N., ADHIKARI S., XIA Y., FENG L.,
RA HARRISON J.K.;
RT *Identification of two rat genes orthologous to the human
interleukin-8 receptors*;
RL J. BIOL. CHEM. 271:32770-32776(1996).
CC -! FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).

DR EMBL; X77797; G498703; -
DR EMBL; D63584; G944819; -
DR EMBL; U70988; G1617613; -
DR PIR; S42096; S42096.
DR GCRDB; GCR 0913; -
DR GCRDB; GCR 1405; -
DR GCRDB; GCR 1524; -
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFM; PFM0001; 7tm.1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
FT CHEMOTAXIS.
FT DOMAIN 1 47
FT TRANSMEM 48 74
FT DOMAIN 75 83
FT TRANSMEM 84 104
FT DOMAIN 105 119
FT TRANSMEM 120 141
FT DOMAIN 142 162
FT TRANSMEM 163 182
FT DOMAIN 183 207
FT TRANSMEM 208 230
FT DOMAIN 231 250
FT TRANSMEM 251 272
FT DOMAIN 273 296
FT TRANSMEM 297 314
FT DOMAIN 315 359
FT CARBOHYD 8 8
FT CARBOHYD 23 23
FT CARBOHYD 201 201
FT CARBOHYD 202 202
FT DISULFID 118 195
SQ SEQUENCE 359 AA; 40532 MW; 5B29D194 CRC32;

Query Match 31.8%; Score 581.5; DB 1; Length 359;
Best Local Similarity 36.6%; Pred. No. 6.1e-33;

Matches 132; Conservative 68; Mismatches 128; Indels 33; Gaps 10;

QY 10 DNYT-EMSGSDYDSMK-----EPCFREANANKIFLPTIYSIIPLTIGVGN 56
 DB DNFSLDFSGSDYDSNYSDDPFTLSDAPC-PSANLDIRAVVYIVYLLSLVGN 65
 QY 57 GLVILVMGQKLRSMTKYRLHLSVADLLFVITLFPMAVDAAVANYFGNLCRAVYIV 116
 DB 66 SLVMTLVILNRSCTSVYDVLNLAIDLFFALTLPVMAASKNGWIFGSLCKVPSFLQ 125
 QY 117 TVNLVSSVLLAFISLDRLAIYHATNSQRPRLKLAEKVYVGVIPALLITPDIIFAN 176
 DB 126 EITPSSVLLACISMDRLAIYHATSTLQKRLV-KVVCITMTWLSVLSPILFRT 184
 QY 177 VSEAD-DRYICDRFPYN-----DLNVVFOFOHIMVGLIPGIVISCYCIISKLSHSHK 230
 DB 185 TVKANPSTVVC--YENIGNNNTSKMRVLRILPOTGIFLLPILMLFCGIFLRTLFKRN 241
 QY 231 GHOKRALATVYLLILAFACMLPYITGISIDSFILLEIKGCEPENTVHKWISITLAL 290
 DB 242 MCKHRAMVIVAVLVLFLLCWPYIVLFTDLMRTKLKKECEHONINKALTEATEIL 301
 QY 291 AEFHCCNLILVAFGAKRTSAQHATSVSRGSSLSKISK--GKRGHSSVSTSESS 347
 DB 302 GFLHSCNLITITAFIGQFR---HGLKIM--ANYGLVSKFELAKGRPSFVSSSANT 355
 QY 348 S 348
 DB 356 S 356

RESULT 13
 CCR3_HUMAN STANDARD: PRT: 368 AA.

AC P49682;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 3 (CXCR-3) (CXCR-3).
 GN CXCR3 OR GPR9.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA.
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RX MEDLINE: 97188912.
 RA LOETSCHER M., GERBER B., LOETSCHER P., JONES S.A., PILLI L.,
 RA CLARK-LEWIS I., BAGGIOLINI M., MOSER B.;
 RT "Chemokine receptor specific for IP10 and mig: structure, function,
 RT and expression in activated T-lymphocytes.";
 RL J. EXP. MED. 184:963-969(1996).
 RN (2)
 RP SEQUENCE OF 5-368 FROM N.A.
 RX MEDLINE: 96115583.
 RA MARCHESE A., HEIBER M., NGUYEN T., HENG H.H.Q., SALLIDIVA V.R.,
 RA CHENG R., MURPHY P.M., TSUI L.-C., SHI X., GREGOR P., GEORGE S.R.,
 RA O'DOWD B.F., DOCHERTY J.M.;
 RT "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
 RT and GPR14, encoding receptors related to interleukin 8, neuropeptide
 RT Y, and somatostatin receptors.";
 RL GENOMICS 29:335-344(1995).
 CC -1- FUNCTION: RECEPTOR FOR IP10 AND MIG.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
 DR EMBL: X95876; E223933;
 DR EMBL: U32674; G1002741;
 DR GCRDB: GCR_1341;
 DR GCRDB: GCR_1972;
 DR MIM: 600894;
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
 DR PFAM: PF00001; 7tm_1; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
 FT DOMAIN 1 53
 FT TRANSMEM 54 80
 FT DOMAIN 81 89
 FT TRANSMEM 90 110
 FT DOMAIN 111 125
 FT TRANSMEM 126 147
 FT DOMAIN 148 169
 FT TRANSMEM 170 189
 FT DOMAIN 190 212
 FT TRANSMEM 213 233
 FT DOMAIN 234 255
 FT TRANSMEM 256 277
 FT DOMAIN 278 298
 FT TRANSMEM 299 321
 FT DOMAIN 322 368
 FT DISULFD 124 203
 FT CARBOHYD 22 22
 FT SEQUENCE 368 AA; 40659 MW; D39A3B6A CRC32;

Query Match 31.5%; Score 576.5; DB 1; Length 368;
 Best Local Similarity 35.0%; Pred. No. 1,4e-32;
 Matches 121; Conservative 70; Mismatches 140; Indels 15; Gaps 4;

QY 10 DNYTEMMSGDYDS-----MKRCPFREANANKIFLPTIYSIIPLTIGVGNGLVILVMGY 65
 DB 21 ENFSSSYDYGENESSCCTSPCCQDFSLNFDRAFLPALSILFLGLLGGNAVAALLS 80
 QY 66 QKLSMTDKYRLHLSVADLLFVITLFPMAVDAAVANYFGNLCRAVYIVTNLYSSVL 125
 DB 81 RRTALSTDTFLHIAVADTLVLTLPMAVDAVAVQWFGSLGVAGALNINIFYAGAL 140
 QY 126 ILAFISLDRLAIYHATNSQRPRLKLAEKVYVGVIPALLITPDIIF--ANYSEADR 183
 DB 141 ILACISFDRLINIVATQVLRGPRPARVTLFCLAWGCLFLALPDLFLSAHDERLNA 200
 QY 184 YICDFYNDLNVVFOFOHIMVGLIPGIVILSCYCIISKLSHSHKORAKLKTIVT 243
 DB 201 THQGVNFP-QVGRPALRVLAQVAGFLPLLVMAVCYAHILAVLLVSRGRLRAMRLVVV 259
 QY 244 ILIAFFACMLPYITGISIDSFILLEIKGCEPENTVHKWISITLALAFPCCLNPILYA 303
 DB 260 VVAVAFALCMTPTYHLVVLVDIIMDLGALARNGRESRVAVKASVSGLGCMCCINPLIYA 319
 QY 304 FLGAKFRTSAQHATSVSRGSSLSKLSKRGHSSVSTSESSSF 349
 DB 320 FVGVFERRMMMLL-----LRIGCPNORGLOROPSSSRDSSW 357

RESULT 14
 IL8B_HUMAN STANDARD: PRT: 360 AA.

AC P25025;
 DT 01-MAY-1992 (REL. 22, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MSGA
 DE RECEPTOR) (IL-8 RECEPTOR TYPE 2).
 GN IL8RB OR CXCR2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN (1)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 14, 1999, 09:51:02; Search time 11.24 Seconds

(Without alignments)
1254.720 Million cell updates/sec

Title: US-09-104-063-4
Perfect score: 1830
Sequence: 1 MEGISITSDNYTEMGSGD.....KRGSHSSVSTSESSSFHSS 352

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database: PIR60:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1830	100.0	352	2	A45747	neuropeptide Y/pep
2	1806	98.7	352	2	G00048	fusin (LESTRA) - c
3	1722.5	94.1	353	2	S28787	neuropeptide Y/pep
4	600.5	32.8	360	2	A57160	chemokine (C-C) re
5	582	31.8	367	2	JE0349	interferon-inducib
6	568	31.0	360	2	A53611	interleukin-8 rece
7	567	31.0	356	2	S42096	interleukin-8 rece
8	564.5	30.8	360	2	UC4587	chemokine (C-C) re
9	564	30.8	355	2	QJ1231	interleukin-8 rece
10	563	30.8	378	2	A57355	G protein-coupled
11	559.5	30.6	350	2	A39445	interleukin-8 rece
12	558	30.5	358	2	A53752	interleukin-8 rece
13	557	30.4	378	2	B55735	lymphocyte-specifi
14	549.5	30.0	355	2	UC4304	orphan G-protein-c
15	544	29.7	327	2	S56162	MDCK15 protein - h
16	540	29.5	372	2	S26667	G protein-coupled
17	539	29.5	359	2	A48921	G protein-coupled
18	538	29.4	378	2	A45680	G protein-coupled
19	536	29.3	374	2	S42688	G protein-coupled
20	533.5	29.2	369	2	UC5068	G protein-coupled
21	529	28.9	374	2	S2785	G protein-coupled
22	528	28.9	374	2	I38450	chemokine (C-C) re
23	527	28.8	355	2	UC5067	G protein-coupled
24	519.5	28.4	383	2	S55594	G protein-coupled
25	514.5	28.1	354	2	I58186	hypothetical G-pro
26	512.5	28.0	360	2	UC2443	chemokine (C-C) re
27	509	27.8	355	2	G02436	C-C chemokine rece
28	507	27.7	355	2	A57237	chemokine (C-C) re
29	506	27.7	352	2	A43113	chemokine (C-C) re
30	503.5	27.5	355	2	A45177	chemokine (C-C) re
31	502.5	27.5	359	2	S15403	angiotensin II rec
32	501.5	27.4	350	2	JN0621	G-protein coupled
33	493.5	27.0	359	2	UC1104	angiotensin II rec
34	493.5	27.0	359	2	A42656	angiotensin II rec
35	488.5	26.7	359	2	S44425	angiotensin II rec
36	487.5	26.6	359	2	J01516	angiotensin II rec
37	485	26.5	362	2	JN0694	angiotensin II rec
38	484.5	26.5	359	2	A48857	Angiotensin II rec
39	483.5	26.4	359	2	JH0621	angiotensin recept

40	481	26.3	359	2	I49341	MIP-1 alpha recept
41	480.5	26.3	359	2	UC2134	angiotensin II rec
42	474.5	25.9	359	2	I39418	angiotensin II typ
43	473.5	25.9	362	2	A30341	G protein-coupled
44	473	25.8	359	2	UC1193	angiotensin II rec
45	472.5	25.8	359	2	UC1194	angiotensin II rec

ALIGNMENTS

RESULT 1
A45747
neuropeptide Y/peptide YY receptor Y3 - human
N:Alternate names: fusin; NH89; leukocyte-derived seven-transmembrane receptor LESTR;
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence revision 03-May-1994 #text change 17-Mar-1999
C:Accession: A45747; A53103; I59444; I59444; I59203; S32761
R:Feederpiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-L
Genomics 16; 707-712, 1993
A:Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a
A:Reference number: A45747; MUID:93315164
A:Accession: A45747
A:Molecule type: mRNA
A:Residues: 1-352 <FEED>
A:Cross-references: GB:M9293; NID:g292516; PID:g292517
R:Loetscher, M.; Geisler, T.; O'Reilly, T.; Zwaehlen, R.; Baggiolini, M.; Moser, B.
J. Biol. Chem. 269, 232-237, 1994
A:Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highl
A:Reference number: A53103; MUID:94103215
A:Accession: A53103
A:Molecule type: mRNA
A:Residues: 1-352 <LOE>
A:Cross-references: EMBL:X71635; NID:g297099; PID:g297100
R:Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A:Title: Molecular cloning, characterization, and localization of the human homolog t
A:Reference number: I53006; MUID:93319629
A:Accession: I53006
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <HER>
A:Cross-references: GB:I06797; NID:g414929; PID:g414928
R:Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salan, J.;
Regul. Pept. 47, 247-258, 1993
A:Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human hom
A:Reference number: I59444; MUID:94052833
A:Accession: I59444
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <RE2>
A:Cross-references: GB:I01639; NID:g189313; PID:g189314
R:Monaur, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte c
A:Reference number: I54751; MUID:94092629
A:Accession: I69203
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <RES>
A:Cross-references: GB:D10924; NID:g219868; PID:g219869
C:Genetics:
A:Gene: GDB:NPY3R; NPY3
A:Cross-references: GDB:230002; OMIM:162643
A:Map position: 2q21-2q21
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 100.0%; Score 1830; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 4 6e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MEGISITSDNYTEMGSGDYDSMKPCFREANFNKIFLPTIYSIIIFLTGIVGNGLVI 60

```

Db      1  MEGISITSDNTYEEEMSGSDYDSMKKEPCFEENANFNKIFLPTIYSITFLTGIVNGLY 60
        61  LVNGYQKRLRSMYDKYRLHLSTVADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVNL 120
        62  LVNGYQKRLRSMYDKYRLHLSTVADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVNL 120
        121 YSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSEA 180
        122 YSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSEA 180
        123 YSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSEA 180
        181 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGKRRALK 240
        182 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGKRRALK 240
        183 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGKRRALK 240
        241 TVLLIAFFACWLPYYIGISIDSFILLEIKGCEFEENTVHKMISTEALAFPHCCINP 300
        242 TVLLIAFFACWLPYYIGISIDSFILLEIKGCEFEENTVHKMISTEALAFPHCCINP 300
        243 TVLLIAFFACWLPYYIGISIDSFILLEIKGCEFEENTVHKMISTEALAFPHCCINP 300
        301 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGHSSTESSESSFHSS 352
        302 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGHSSTESSESSFHSS 352
        303 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGHSSTESSESSFHSS 352

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RESULT 2
G00048
fusion (LESTRA) - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 11-Apr-1997
C:Accession: G00048
R:Atsumi, M.
submitted to GenBank, July 1996
A:Reference number: H00048
A:Accession: G00048
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <TAT>
A:Cross-references: GB:D86579; NID:g1468948; PID:g1468949

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Query Match      98.7%; Score 1806; DB 2; Length 352;
Best Local Similarity 98.3%; Pred. No. 4.3e-141;
Matches 346; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1  MEGISITSDNTYEEEMSGSDYDSMKKEPCFEENANFNKIFLPTIYSITFLTGIVNGLY 60
        1  MEGISITSDNTYEEEMSGSDYDSMKKEPCFEENANFNKIFLPTIYSITFLTGIVNGLY 60
        61  LVNGYQKRLRSMYDKYRLHLSTVADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVNL 120
        62  LVNGYQKRLRSMYDKYRLHLSTVADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVNL 120
        63  LVNGYQKRLRSMYDKYRLHLSTVADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVNL 120
        121 YSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSEA 180
        122 YSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSEA 180
        123 YSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSEA 180
        181 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGKRRALK 240
        182 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGKRRALK 240
        183 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGKRRALK 240
        241 TVLLIAFFACWLPYYIGISIDSFILLEIKGCEFEENTVHKMISTEALAFPHCCINP 300
        242 TVLLIAFFACWLPYYIGISIDSFILLEIKGCEFEENTVHKMISTEALAFPHCCINP 300
        243 TVLLIAFFACWLPYYIGISIDSFILLEIKGCEFEENTVHKMISTEALAFPHCCINP 300
        301 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGHSSTESSESSFHSS 352
        302 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGHSSTESSESSFHSS 352
        303 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGHSSTESSESSFHSS 352

```

RESULT 3
 S28787
 neuropeptide Y/peptide YY receptor Y3 - bovine
 C:Species: Bos primigenius taurus (cattle)

```

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 06-Dec-1996
C:Accession: S28787
R:Rimland, J.; Xin, W.; Sweetnam, P.; Saljoh, K.; Nestler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A>Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A:Reference number: S28787; MUID:92100053
A:Accession: S28787
A:Molecule type: mRNA
A:Residues: 1-353 <RIM>
A:Cross-references: EMBL:M86739
C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

```

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Query Match      94.1%; Score 1722.5; DB 2; Length 353;
Best Local Similarity 92.4%; Pred. No. 3.1e-134;
Matches 326; Conservative 20; Mismatches 6; Indels 1; Gaps 1;

QY      1  MEGISITSDNTYEEEMSGSDYDSMKKEPCFEENANFNKIFLPTIYSITFLTGIVNGLY 59
        1  MEGISITSDNTYEEEMSGSDYDSMKKEPCFEENANFNKIFLPTIYSITFLTGIVNGLY 60
        61  LVNGYQKRLRSMYDKYRLHLSTVADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVN 119
        62  LVNGYQKRLRSMYDKYRLHLSTVADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVN 119
        63  LVNGYQKRLRSMYDKYRLHLSTVADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVN 119
        120 LVSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSE 179
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        180 ADDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGKRRALK 239
        181 VDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGKRRALK 240
        182 VDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGKRRALK 240
        241 TVLLIAFFACWLPYYIGISIDSFILLEIKGCEFEENTVHKMISTEALAFPHCCINP 300
        242 TVLLIAFFACWLPYYIGISIDSFILLEIKGCEFEENTVHKMISTEALAFPHCCINP 300
        243 TVLLIAFFACWLPYYIGISIDSFILLEIKGCEFEENTVHKMISTEALAFPHCCINP 300
        300 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGHSSTESSESSFHSS 352
        301 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGHSSTESSESSFHSS 353
        302 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGHSSTESSESSFHSS 353

```

```

RESULT 4
A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
J. Biol. Chem. 270, 19495-19500, 1995
A>Title: Molecular cloning and functional expression of a novel CC chemokine receptor
A:Reference number: A57160; MUID:95370289
A:Accession: A57160
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POW>
A:Cross-references: GB:X85740; NID:g1370103; PID:g9711452
A:Note: source clone K5-5
C:Genetics:
A:Gene: GDB:CMKBR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:40-65/Domain: transmembrane #status predicted <TM>
F:76-97/Domain: transmembrane #status predicted <TM>
F:112-133/Domain: transmembrane #status predicted <TM>
F:151-175/Domain: transmembrane #status predicted <TM>
F:208-226/Domain: transmembrane #status predicted <TM>
F:243-264/Domain: transmembrane #status predicted <TM>
F:291-308/Domain: transmembrane #status predicted <TM>
F:29-276,110-187/disulfide bonds: #status predicted
F:72,350/binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predi

```


QY 289 AALAFHCLNPLIYAFGLGAKFKTSQAQHALTSVRSGLSLKSGKRGHSSTES----- 345
 Db 301 ILGLHSCNLPILYAFIGQKFR-----HGL-----LKILAI-----HGLISKDSLPRD 343
 QY 345 -----ESSFHS 352
 Db 344 SRPSEVSGSSGHTS 357

RESULT 7

interleukin-8 receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Feb-1997
 C:Accession: S42096
 R:Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
 submitted to the EMBL Data Library, February 1994
 A:Description: Molecular cloning of the rat IL8 receptor.
 A:Reference number: S42096
 A:Accession: S42096
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-356 <GOB>
 A:Cross-references: EMBL:X77797
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 31.0%; Score 567; DB 2; Length 356;
 Best Local Similarity 36.3%; Pred. No. 2e-39;
 Matches 131; Conservative 68; Mismatches 126; Indels 36; Gaps 11;

QY 10 DNYT-EEMSGSDYDSM-----EPCFREANFNKIFLPTIYSIIFLGIYGN 56
 Db 7 DNFSLEDFSGDIDYNSDPFETLSDAAPC-PSANLDINRYAVVYIVLTLSLIGN 65
 QY 57 GLVITVMGYCKLRSMTRYRLHLSVADLVYITLPFAVDVAVNMYGNFLCAVHYI 116
 Db 66 SLVMTVILYNSTGCVTVYVILNLAIADLFALPVAASKVNGMIGSFLCKVFSFLQ 125
 QY 117 TVNIYSSVILAFISLDRLAIVHATNSORPKLLAEKVYVGVWIPALLTIPDIFRAN 176
 Db 126 EITFYSSVLLACISMRYLAIVHATSLIQRHLY-KFVCITMWSFLVSLPFIIRT 184
 QY 177 VSEAD-DRYICDRYPN-----DLWVVFQFOHIMWGLIPGIYILSCYCIITKLSHK 230
 Db 185 TVKANPSTVVC---YENIGNNTSKRWVLRILPQYGFLLPLMLFCYGFTRFLFRAN 241
 QY 231 GHOKRAKKTIVILIAFAACMLPYIGISIDSFILFETIKOGCEFEVTVKATISTEAL 290
 Db 242 MGQHRRAKRVIFAVLVFLDLPYIVLEFDTLMRKRLKETGERONEIK---ASEIL 298
 QY 291 AFPHCLNPLIYAFGLGAKFKTSQAQHALTSVRSGLSLKSK---GKRGHSSTESPS 347
 Db 299 GLHSCNLPILYAFIGQKFR-----HGLIKIM--ANYGLVSKFLAKESRPFSVSSSANT 352
 QY 348 S 348
 Db 353 S 353

RESULT 8

chemokine (C-C) receptor 4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 12-Dec-1997
 C:Accession: J04587
 R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996
 A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A:Reference number: J04587
 A:Accession: J04587
 A:Molecule type: mRNA

A:Residues: 1-360 <HOO>
 A:Cross-references: EMBL:X00862; NID:g1167851; PID:e195632; PID:g1167852
 A:Experimental source: thymus
 C:Genetics:

A:Gene: cc ckr-4
 C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F:2,183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status p
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predi

Query Match 30.8%; Score 564.5; DB 2; Length 360;
 Best Local Similarity 37.3%; Pred. No. 3.3e-39;
 Matches 109; Conservative 63; Mismatches 117; Indels 3; Gaps 2;

QY 21 YDSKKEPCFREANFNKIFLPTIYSIIFLGIYGNGLVILVNGYOKLRSMTRYRLH 80
 Db 22 YESMPKCTKRGKIFAGFEVLPPLYSIVFLGLFGNSVVVLVLFKRYKLSMTDVIYLN 81
 QY 81 SVADLVITLPFAVDVAVNMYGNFLCAVHYITVNIYSSVILAFISLDRLAIVH 140
 Db 82 AISDLFVLSPFWGYAADQWVFGGLCKIVSMYLVGFSGIFIMLSIDRYLAIVH 141
 QY 141 ATNSORPKLLAEKVYVGVWIPALLTIPDIFANVSEADDRYICDRYP--NDLWVY 198
 Db 142 AVFSLKARITLYGYITSLITMSVAVFASLPGLFSTCYTEHNTCTQYSVNSTWKVL 201
 QY 199 FQFOHIMWGLIPGIYILSCYCIITKLSHSGHOKRAKKTIVILIAFAACWPEYIIG 258
 Db 202 SLEINVLGLIPGIMLFYSMIIRTLQCKNEKKRAVRMIFGVVLELFGWTPYNV 261
 QY 259 ISIDFILLFETIKOGCEFEVTVKATISTEALAFPHCLNPLIYAFGLGAKFK 310
 Db 262 LFLFETLVEVL-QDCTLEKRYLDIAQATETLGFHCLNPLIYFFLGEXER 312

RESULT 9

interleukin-8 receptor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Mar-1998
 C:Accession: J01231; A46483
 R:Beckmann, M.P.; Manger, W.E.; Kozlosky, C.; Vandenbos, T.; Price, V.; Lyman, S.; Ge
 Biochem. Biophys. Res. Commun. 179, 784-789, 1991
 A:Title: Molecular characterization of the interleukin-8 receptor.
 A:Reference number: J01231; M01D:91378994
 A:Accession: J01231
 A:Molecule type: DNA
 A:Residues: 1-355 <BEC>
 A:Cross-references: GB:M74240; NID:g165438; PID:g165439
 R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
 J. Immunol. 148, 1261-1264, 1992
 A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 recept
 A:Reference number: A46483; M01D:92148149
 A:Accession: A46483
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-355 <LEE>
 A:Cross-references: GB:M82873; NID:g165440; PID:g165441
 A:Experimental source: neutrophils
 A:Note: Sequence extracted from NCBI backbone (NCBIN:81526, NCBI:81530)
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 30.8%; Score 564; DB 2; Length 355;
 Best Local Similarity 35.0%; Pred. No. 3.6e-39;
 Matches 123; Conservative 71; Mismatches 149; Indels 8; Gaps 6;

QY 1 MEGISITYSDNYEEMSGSDYDSMKPCFREANFNKIFLPTIYSIIFLGIYGNGLVI 60
 Db 8 MTDLMTWTFEDERANATGMPVENDYSPCL-VYTQTLNKIVVIVYALVFLSLGNSLVM 66

[illegible]

RESULT 10
A55735
G Protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 17-Mar-1999
C:Accession: A55735
R:Schweikardt, V.L.; Rapport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735, MUID:95154835
A:Accession: A55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:LJ1580; NID:q468340; PID:q468341
A:Keywords: G protein-coupled receptor

[illegible]

RESULT 11
A39445
interleukin-8 receptor type A - human
N:Alternate names: interleukin-8 receptor, high-affinity
C:Species: Homo sapiens (man)

C>Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 24-Sep-1998
C:Accession: I37449; I38710; I38711; A39445
R:Morelleau, C.; Muscatelli, F.; Matteli, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993
A>Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the
A:Reference number: I37449; MIMD:9352387
A:Accession: I37449

A:Cross-references: EMBL:X65858; NID:G312046; PID:G312047
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human inter-
A:Reference number: 137858; MUID:95014476
A:Accession: 138710
A:Molecule type: DNA
A:Residues: 1-350 <REZ>
A:Cross-references: EMBL:U11870; NID:G511804; PID:G511805
A:Accession: 138711
A:Molecule type: mRNA
A:Residues: 1-16 <RE3>
A:Cross-references: EMBL:U11871; NID:G511806; PID:G733002
R:Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A:Title: Structure and functional expression of a human interleukin-8 receptor.
A:Reference number: A39445; MUID:91368193
A:Accession: A39445
A:Molecule type: mRNA
A:Residues: 1-275, 'T', 277-350 <HOL>
A:Cross-references: GB:M68932; NID:G186369; PID:G186370
C:Genetics:
A:Gene: GDB:IL8RA
A:Cross-references: GDB:135039; OMIM:146929
A:Map position: 2q35-2q35
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match	30.6%	Score 559.5	DB 2	Length 350:	
Best Local Similarity	38.2%	Pred. No. 8.2e-39			
Matches 121:	Conservative	56:	Mismatches 127:	Indels 13:	Gaps 6:
Db	11	NYTEEMSGSDVYSMKPEPFREENANFNKIFLPITYSIIFFLTGIVNGAVILVMGYOKRLR	70		
Db	16	NFT---GMPRADEDSPCM-L-ETETLNKTVYIAIALVFLSLTGNLSMLVYLISRGR	71		
QY	71	SMTDKYRLHLVSADILEVYITLPFMAVDAAVMNYFCGNFLCKAVHYIYTVNLSSVZILAFI	130		
Db	72	SVTDVYLLNTLALADLLFALTLPLPIMASRVNGMIFGTCPLCKVYSLKEVNFYSGIILLACI	131		
QY	131	SUDRIALAVHATNSGRPKLLAEKVVYVGWLPALLLIIPDTIFANVSADRY-ICDRE	189		
Db	132	SVDRILAVHATRIITLQKRLHLV-KFVCCGCMGLSNMLSPFLFPGQAAVHPNNSSEVCEY	190		
QY	190	YPNDL--WVWVFOFHIMWGILPGLVILSCYIIISKLSHSGHOKRKALTYVILILA	247		
Db	191	LGNDAKRRMVLRIPLPHFGFIVLPFLVWLPCTGFLRLIRFKAHMQOKHRAMAVYTRAVVLT	250		
QY	248	EFACMLPYIYIGISIDSFILLETIIKOGCEFEENTVHKWISITTEALAFHCCILNITLYAFIGA	307		
Db	251	FLLCWLPYNLVILADTLRTQYIDQSCRRNNIGALDATALTELGLHSCNLNPIYAFIQ	310		
QY	308	KF-----KTSQHALTS	319		
Db	311	NFRHGFLKILAMHGLVVS	327		

RESULT 12
A53752
interleukin-8 receptor (clone 5B1a) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997
C:Accession: A53752
C:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Nava

J. Biol. Chem 269, 12391-12394, 1994
A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype-A:Reference number: A53752, MUID:94230294
A:Accession: A53752
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-358 <PRA>
A:Cross-references: GB:L24445, NID:g437661, PID:g437662
A:Keywords: G protein-coupled receptor; transmembrane protein

[illegible]

RESULT 13
B55735
Lymphocyte-specific G-protein-coupled receptor EB11 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 17-Mar-1999
C:Accession: B55735 #S52443
R:Schneidart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835
A:Accession: B55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <GB>
A:Cross-references: GB:L31581; NID:q468319; PID:q468320
R:Burgstahler, R.; Kempkes, B.; Staebde, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically transre-
A:Reference number: S52443
A:Accession: S52443
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 21-378 <BUR>
A:Cross-references: EMBL:X84702
C:Genetics:
A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7
A:Cross-references: GDB:342065; OMIM:600242
A:Map position: 1/q12-1/q21.2

C;Keywords: G protein-coupled receptor

[illegible]

```

RESULT 14
JC4304
Orphan G-protein-coupled receptor - human
N:Alternate names: V28 protein
C:Species: Homo sapiens (man)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 17-Mar-1999
C:Accession: JC4304
R:Report: C.J.; Schweikart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to
A:Reference number: JC4304; MUID:96011651
A:Accession: JC4304
A:Molecule type: mRNA
A:Residues: 1-355 <RAP>
A:Cross-references: GB:U20350; NID:g665580; PID:g665581
A:Experimental source: peripheral blood mononuclear cell
C:Comment: This protein is a cell-surface receptor which recognizes extracellular signals
C:Comment: This protein is a key regulator of many immune and homeostatic responses,
C:Genetics:
A:Gene: V28
A:Map position: 3pter-p21
C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F:35-57/Domain: transmembrane #status predicted <TM1>
F:66-88/Domain: transmembrane #status predicted <TM2>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>

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	Query Match	30.0%	Score 549.5.	DB-2:	Length 355:
	Best Local Similarity	33.2%	Pred.No.5e-38;		
	Matches 119; Conservative	68;	Mismatches 144;	IndeIs	Gaps 77;
OY	DNTTEKMGSG-DVDSMKKEPCFRENANENKFELPTISIIIFLTGIVNGVLIMYOQKK	68			
	: - : : : : : : : : :				
Db	LDPPESTETNEFEVDLLAEACYIGIDIAVFEGTFLSIFYSVIFAIGLVGNLVAFFALTNSSK	61			
OY	LRSMTDKRIHLHSLADLLVIITLPFAAVDAVANWNYIGNLCRAHVHYTVVNLYSSLILA	128			
	: :: : : :: : :	:	:: :	:	:

Db 62 PKSVTDIYLLNMTASDLLFVATLTFPMTHYILNKGHLNMAKCFITAAFFIGFGSIFETI 121

Qy 129 FISIDRYALAIYHAINSQRPRLKLEKVVYGVWTFPALLLITPDPFIPANSEADRIYICOR 188

Db 122 VISIDRYALAIYLAANSMMNRVQHGVTISLGWMAAILVAPQFMFKRENE----CLG 177

Qy 189 FYP--NDLAWVEFOFOHIMVGLILPGVILSCYIIISKLSKSGHOKRKALKTIVIT 245

Db 178 DYPEVLQGIWVLANVEINELFGFLLPRLIMSYCYFRIIQTLLPSCKHNKKAKAKILLVY 237

Qy 246 LAFAACWLPIYIGISIDSFILLEIITIKOGCEFEENTVHKMWISITALEAFHCOLPILAYEL 305

Db 238 IYVLEFLMYPYVMWIFLETLLKYDFE--PSCDMRKDLRLATSVETEVAFVSHCCLPILYAF 296

Qy 306 GAKFETSAQHLLSVSGSSKLIL-----SKRGKGHSVSTEBESSFHS 352

Db 297 GEFKRRYIYILY-----GKCLAVLCGSHVHDESSSSQSRGSGVY--SSNTYHTS 347

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 14, 1999, 09:51:02 : Search time 23.15 Seconds
(without alignments)
864.389 Million cell updates/sec

Title: US-09-104-063-4
1830
Perfect score: 1 MEGISITSDMYTEMGSGD.....KRGHSVSTSESSSFHSS 352
Sequence:

Scoring table: BLOSUM62

Searched: 453288 segs, 56848278 residues

Database :

Pending Patents, AA:*

1: /cgn2_6/ptodata/2/paa/PCTUS9.COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US07.COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US080.COMB.pep.*
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7: /cgn2_6/ptodata/2/paa/US084.COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084B.COMB.pep.*
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23: /cgn2_6/ptodata/1/paa/US60_NEW.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1830	100.0	352	1	PCT-US93-10672-2	Sequence 2, Appl1
2	1830	100.0	352	6	US-08-308-880-2	Sequence 2, Appl1
3	1830	100.0	352	7	US-08-441-562-2	Sequence 2, Appl1
4	1830	100.0	352	12	US-08-801-228-4	Sequence 4, Appl1
5	1830	100.0	352	12	US-08-801-228-4	Sequence 4, Appl1
6	1830	100.0	352	12	US-08-802-627-4	Sequence 4, Appl1
7	1830	100.0	352	12	US-08-802-627-4	Sequence 4, Appl1
8	1830	100.0	352	15	US-09-104-063-4	Sequence 4, Appl1
9	1830	100.0	352	15	US-09-104-063-4	Sequence 4, Appl1
10	1808	98.8	356	15	US-09-122-068-2	Sequence 4, Appl1
11	1789	97.8	352	4	US-08-182-962-6	Sequence 6, Appl1
12	1789	97.8	352	7	US-08-446-669-6	Sequence 6, Appl1
13	1789	97.8	352	7	US-08-450-393-6	Sequence 6, Appl1
14	1752	95.7	337	2	US-07-977-452A-21	Sequence 6, Appl1
15	1752	95.7	337	2	US-08-245-242-46	Sequence 21, Appl1
16	1752	95.7	337	22	US-09-299-843A-46	Sequence 46, Appl1
17	600.5	32.8	360	10	US-08-675-814-14	Sequence 14, Appl1
18	600.5	32.8	360	12	US-08-875-573-20	Sequence 20, Appl1
19	600.5	32.8	360	12	US-08-887-977-16	Sequence 16, Appl1
20	600.5	32.8	360	13	US-08-989-107-34	Sequence 34, Appl1

21	600.5	32.8	360	14	US-09-045-593-55	Sequence 55, Appl1
22	600.5	32.8	360	14	US-09-067-447-34	Sequence 34, Appl1
23	600.5	32.8	360	14	US-09-067-447-34	Sequence 34, Appl1
24	600.5	32.8	360	16	US-09-232-878-2	Sequence 2, Appl1
25	594	32.5	123	9	US-08-513-974B-330	Sequence 330, App
26	588.5	32.2	360	12	US-08-833-752-10	Sequence 10, Appl1
27	576.5	31.5	368	11	US-08-709-838-2	Sequence 2, Appl1
28	576.5	31.5	368	12	US-08-829-839-2	Sequence 2, Appl1
29	568	31.0	355	1	PCT-US93-10672-4	Sequence 4, Appl1
30	568	31.0	353	1	PCT-US96-00499-9	Sequence 9, Appl1
31	568	31.0	353	1	PCT-US96-00499A-9	Sequence 9, Appl1
32	568	31.0	355	4	US-08-182-962-8	Sequence 8, Appl1
33	568	31.0	355	6	US-08-308-880-4	Sequence 4, Appl1
34	568	31.0	355	6	US-08-390-000A-5	Sequence 5, Appl1
35	568	31.0	355	7	US-08-441-562-4	Sequence 4, Appl1
36	568	31.0	355	7	US-08-446-669-8	Sequence 8, Appl1
37	568	31.0	355	7	US-08-450-393-8	Sequence 8, Appl1
38	568	31.0	165	10	US-08-605-185-22	Sequence 22, Appl1
39	568	31.0	360	16	US-09-236-166-4	Sequence 4, Appl1
40	567.5	31.0	415	1	PCT-US96-00499-2	Sequence 2, Appl1
41	567.5	31.0	415	1	PCT-US96-00499A-2	Sequence 2, Appl1
42	563	30.8	378	5	US-08-245-242-66	Sequence 66, Appl1
43	563	30.8	378	22	US-09-299-843A-66	Sequence 66, Appl1
44	557.5	30.5	350	1	PCT-US93-10672-3	Sequence 3, Appl1
45	557.5	30.5	350	1	PCT-US99-11842-27	Sequence 27, Appl1

ALIGNMENTS

RESULT 1

PCT-US93-10672-2

Sequence 2, Application PC/TUS9310672

GENERAL INFORMATION:

APPLICANT: GENENTECH, INC.

TITLE OF INVENTION: CC-CHEMOKINE RECEPTOR

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patia (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10672

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Pitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 806

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1489

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US93-10672-2

Query Match 100.0%; Score 1830; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 2, 1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MEGISITSDNNTYEMGSGDYDSMKKEPCFRENNANFKITLPTIYISITFLGTIVGNGLVI 60
    |||
DB 1 MEGISITSDNNTYEMGSGDYDSMKKEPCFRENNANFKITLPTIYISITFLGTIVGNGLVI 60
    |||
OY 61 LVNGYOKKLKSMPTDKYRLHLHSVADLLFVITLPPWADAVANWVFGNLCRAVHIYTVNL 120
    |||
DB 61 LVNGYOKKLKSMPTDKYRLHLHSVADLLFVITLPPWADAVANWVFGNLCRAVHIYTVNL 120
    |||
OY 121 YSSVLLIAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLTITDFIFANVSEA 180
    |||
DB 121 YSSVLLIAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLTITDFIFANVSEA 180
    |||
OY 181 DDRYICDREYNDLWVYVFOFHIMWGLIPGIYILSCYCIITISKLSHSGHOKRKALKT 240
    |||
DB 181 DDRYICDREYNDLWVYVFOFHIMWGLIPGIYILSCYCIITISKLSHSGHOKRKALKT 240
    |||
OY 241 TVLLILAFACWLPYYIGISIDSFILLEITKOGCEPENTVHKWISTEALAFHCCLNPI 300
    |||
DB 241 TVLLILAFACWLPYYIGISIDSFILLEITKOGCEPENTVHKWISTEALAFHCCLNPI 300
    |||
OY 301 LVAFLEAKFTSAQHALLTSVRGSSSLKILSKRGKGSVSTESSESSFHSS 352
    |||
DB 301 LVAFLEAKFTSAQHALLTSVRGSSSLKILSKRGKGSVSTESSESSFHSS 352
    |||
```

RESULT 2
US-08-308-880-2
; Sequence 2, Application US/08308880
; GENERAL INFORMATION:

APPLICANT: RICHARD HORUK, KULDEEP NEOTE, THOMAS SCHALL
TITLE OF INVENTION: CC-CHEMOKINE RECEPTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,880
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/974025
FILING DATE: 10-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-308-880-2

Query Match 100.0%; Score 1830; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2, 1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MEGISITSDNNTYEMGSGDYDSMKKEPCFRENNANFKITLPTIYISITFLGTIVGNGLVI 60
    |||
DB 1 MEGISITSDNNTYEMGSGDYDSMKKEPCFRENNANFKITLPTIYISITFLGTIVGNGLVI 60
    |||
OY 61 LVNGYOKKLKSMPTDKYRLHLHSVADLLFVITLPPWADAVANWVFGNLCRAVHIYTVNL 120
    |||
DB 61 LVNGYOKKLKSMPTDKYRLHLHSVADLLFVITLPPWADAVANWVFGNLCRAVHIYTVNL 120
    |||
OY 121 YSSVLLIAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLTITDFIFANVSEA 180
    |||
DB 121 YSSVLLIAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLTITDFIFANVSEA 180
    |||
OY 181 DDRYICDREYNDLWVYVFOFHIMWGLIPGIYILSCYCIITISKLSHSGHOKRKALKT 240
    |||
DB 181 DDRYICDREYNDLWVYVFOFHIMWGLIPGIYILSCYCIITISKLSHSGHOKRKALKT 240
    |||
OY 241 TVLLILAFACWLPYYIGISIDSFILLEITKOGCEPENTVHKWISTEALAFHCCLNPI 300
    |||
DB 241 TVLLILAFACWLPYYIGISIDSFILLEITKOGCEPENTVHKWISTEALAFHCCLNPI 300
    |||
OY 301 LVAFLEAKFTSAQHALLTSVRGSSSLKILSKRGKGSVSTESSESSFHSS 352
    |||
DB 301 LVAFLEAKFTSAQHALLTSVRGSSSLKILSKRGKGSVSTESSESSFHSS 352
    |||
```

RESULT 3
US-08-441-562-2
; Sequence 2, Application US/08441562
; GENERAL INFORMATION:

APPLICANT: RICHARD HORUK, KULDEEP NEOTE, THOMAS SCHALL
TITLE OF INVENTION: Nucleic Acids Encoding C-C Chemokine Receptor
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,562
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/308880
FILING DATE: 19-SEP-1994
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 07/974025
FILING DATE: 10-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0806C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-441-562-2

Query Match 100.0%; Score 1830; DB 7; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MEGISITSDNYTEEMSGDYDSMKKEPCFRENNANFNKIFLPTIYSIIFLTGIVGNGLVI 60
    |||||||
DB 1 MEGISITSDNYTEEMSGDYDSMKKEPCFRENNANFNKIFLPTIYSIIFLTGIVGNGLVI 60
    |||||||
QY 61 LVMGYOKRLSMMDKYRLHLSVADLLFVITLPEFAVDVAVANWYGFNGLCAVAVHYITVNL 120
    |||||||
DB 61 LVMGYOKRLSMMDKYRLHLSVADLLFVITLPEFAVDVAVANWYGFNGLCAVAVHYITVNL 120
    |||||||
QY 121 YSSVLIATSLDRYLAIIVATNSQRPRLAEKVYVGVWIPALLTIPDFIFANVSEA 180
    |||||||
DB 121 YSSVLIATSLDRYLAIIVATNSQRPRLAEKVYVGVWIPALLTIPDFIFANVSEA 180
    |||||||
QY 181 DDRYICDRFPNDLMVYVFOQHIMVGLLPGIYILSCYCIISKLSHSGHOKRKALKT 240
    |||||||
DB 181 DDRYICDRFPNDLMVYVFOQHIMVGLLPGIYILSCYCIISKLSHSGHOKRKALKT 240
    |||||||
QY 241 TVIIILAFACWLPYYIGISIDSFILLEIIOGCEFEFNTYHKWISTEALAFHCCLNPI 300
    |||||||
DB 241 TVIIILAFACWLPYYIGISIDSFILLEIIOGCEFEFNTYHKWISTEALAFHCCLNPI 300
    |||||||
QY 301 LYAFLGAKFKTSAQHALTYSRGSLSKILSKGRGHSVSTESSESSFHSS 352
    |||||||
DB 301 LYAFLGAKFKTSAQHALTYSRGSLSKILSKGRGHSVSTESSESSFHSS 352
    |||||||

```

RESULT 4
US-08-801-228-4
; Sequence 4, Application US/08801228
; GENERAL INFORMATION:

```

; APPLICANT: Wood, William I.
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,228
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids

```

; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-801-228-4

Query Match 100.0%; Score 1830; DB 12; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MEGISITSDNYTEEMSGDYDSMKKEPCFRENNANFNKIFLPTIYSIIFLTGIVGNGLVI 60
    |||||||
DB 1 MEGISITSDNYTEEMSGDYDSMKKEPCFRENNANFNKIFLPTIYSIIFLTGIVGNGLVI 60
    |||||||
QY 61 LVMGYOKRLSMMDKYRLHLSVADLLFVITLPEFAVDVAVANWYGFNGLCAVAVHYITVNL 120
    |||||||
DB 61 LVMGYOKRLSMMDKYRLHLSVADLLFVITLPEFAVDVAVANWYGFNGLCAVAVHYITVNL 120
    |||||||
QY 121 YSSVLIATSLDRYLAIIVATNSQRPRLAEKVYVGVWIPALLTIPDFIFANVSEA 180
    |||||||
DB 121 YSSVLIATSLDRYLAIIVATNSQRPRLAEKVYVGVWIPALLTIPDFIFANVSEA 180
    |||||||
QY 181 DDRYICDRFPNDLMVYVFOQHIMVGLLPGIYILSCYCIISKLSHSGHOKRKALKT 240
    |||||||
DB 181 DDRYICDRFPNDLMVYVFOQHIMVGLLPGIYILSCYCIISKLSHSGHOKRKALKT 240
    |||||||
QY 241 TVIIILAFACWLPYYIGISIDSFILLEIIOGCEFEFNTYHKWISTEALAFHCCLNPI 300
    |||||||
DB 241 TVIIILAFACWLPYYIGISIDSFILLEIIOGCEFEFNTYHKWISTEALAFHCCLNPI 300
    |||||||
QY 301 LYAFLGAKFKTSAQHALTYSRGSLSKILSKGRGHSVSTESSESSFHSS 352
    |||||||
DB 301 LYAFLGAKFKTSAQHALTYSRGSLSKILSKGRGHSVSTESSESSFHSS 352
    |||||||

```

RESULT 5

US-08-801-238-4
; Sequence 4, Application US/08801238
; GENERAL INFORMATION:

```

; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881

```

TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-801-238-4

Query Match 100.0%; Score 1830; DB 12; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.1e-167;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGSIYTSNDYTEEMSGDYDSKMEPCFRENNANFNKIFLPTIYSIIFLGIYNGLYI 60
 DB 1 MEGSIYTSNDYTEEMSGDYDSKMEPCFRENNANFNKIFLPTIYSIIFLGIYNGLYI 60
 QY 61 LVMGYQKKLRSMYDKYRLHLSVADLLFVITLPEWADVAVANWYFGNPLCKAVHYITVNL 120
 DB 61 LVMGYQKKLRSMYDKYRLHLSVADLLFVITLPEWADVAVANWYFGNPLCKAVHYITVNL 120
 QY 121 YSSVLLIAFLSLDRYLAVHATNSORPRKLLAEKVYVGVWIPALLTIPOPIFANVSEA 180
 DB 121 YSSVLLIAFLSLDRYLAVHATNSORPRKLLAEKVYVGVWIPALLTIPOPIFANVSEA 180
 QY 181 DDRYICDRFYNDLMVYVFOQHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
 DB 181 DDRYICDRFYNDLMVYVFOQHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
 QY 241 TVIILAFACMLPYIIGISIDSFILLEIKOGCEFEYVHKWISITBALAFHCCLNPI 300
 DB 241 TVIILAFACMLPYIIGISIDSFILLEIKOGCEFEYVHKWISITBALAFHCCLNPI 300
 QY 301 LYAFLGAKFKTSAQHALLTVSRGSSLKILSKGRGHSSVSTESSSPHSS 352
 DB 301 LYAFLGAKFKTSAQHALLTVSRGSSLKILSKGRGHSSVSTESSSPHSS 352

RESULT 6

US-08-802-627-4
 Sequence 4, Application US/08802627

GENERAL INFORMATION:
 APPLICANT: Lee, James
 TITLE OF INVENTION: NUCLEIC ACID ENCODING PFAA RECEPTOR
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Gentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Gentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/802.627
 FILING DATE: 19-Feb-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/284586
 FILING DATE: 10-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/076093
 FILING DATE: 11-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P07062P1D2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-802-627-4

Query Match 100.0%; Score 1830; DB 12; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.1e-167;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGSIYTSNDYTEEMSGDYDSKMEPCFRENNANFNKIFLPTIYSIIFLGIYNGLYI 60
 DB 1 MEGSIYTSNDYTEEMSGDYDSKMEPCFRENNANFNKIFLPTIYSIIFLGIYNGLYI 60
 QY 61 LVMGYQKKLRSMYDKYRLHLSVADLLFVITLPEWADVAVANWYFGNPLCKAVHYITVNL 120
 DB 61 LVMGYQKKLRSMYDKYRLHLSVADLLFVITLPEWADVAVANWYFGNPLCKAVHYITVNL 120
 QY 121 YSSVLLIAFLSLDRYLAVHATNSORPRKLLAEKVYVGVWIPALLTIPOPIFANVSEA 180
 DB 121 YSSVLLIAFLSLDRYLAVHATNSORPRKLLAEKVYVGVWIPALLTIPOPIFANVSEA 180
 QY 181 DDRYICDRFYNDLMVYVFOQHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
 DB 181 DDRYICDRFYNDLMVYVFOQHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
 QY 241 TVIILAFACMLPYIIGISIDSFILLEIKOGCEFEYVHKWISITBALAFHCCLNPI 300
 DB 241 TVIILAFACMLPYIIGISIDSFILLEIKOGCEFEYVHKWISITBALAFHCCLNPI 300
 QY 301 LYAFLGAKFKTSAQHALLTVSRGSSLKILSKGRGHSSVSTESSSPHSS 352
 DB 301 LYAFLGAKFKTSAQHALLTVSRGSSLKILSKGRGHSSVSTESSSPHSS 352

RESULT 7

US-08-802-627A-4
 Sequence 4, Application US/08802627A

GENERAL INFORMATION:
 APPLICANT: Lee, James
 TITLE OF INVENTION: NUCLEIC ACID ENCODING PFAA RECEPTOR
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Gentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Gentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/802.627A
 FILING DATE: 19-Feb-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/284586
 FILING DATE: 10-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/076093

FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-9530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-802-6274-4

Query Match 100.0%; Score 1830; DB 12; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITSDNYTEEMSGDYSKKEPCFRENNANFNKIFLPTIYSITFLTGIVNGLYI 60
DB 1 MEGISITSDNYTEEMSGDYSKKEPCFRENNANFNKIFLPTIYSITFLTGIVNGLYI 60
QY 61 LVMGYOKKLSMTDKYRLHLSVADLLEFVITLPEWADVAVANWYGFNLCRAVHYTYVNL 120
DB 61 LVMGYOKKLSMTDKYRLHLSVADLLEFVITLPEWADVAVANWYGFNLCRAVHYTYVNL 120
QY 121 YSSVLLIAFSLDRIYLAIVHATNSQRPKLLAEKVYVYGVWIPALLTIPDFIFANVSEA 180
DB 121 YSSVLLIAFSLDRIYLAIVHATNSQRPKLLAEKVYVYGVWIPALLTIPDFIFANVSEA 180
QY 181 DDRYICDRFYNDLWVYVFOFOHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
DB 181 DDRYICDRFYNDLWVYVFOFOHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
QY 241 TVIIILAFACWLPYIYGISIDSFILLEIKOGCEFEVTYHKMISTEALAFHCCCLNPI 300
DB 241 TVIIILAFACWLPYIYGISIDSFILLEIKOGCEFEVTYHKMISTEALAFHCCCLNPI 300
QY 301 LYAFLAGKFTSAQHATLSVRSGLKILSKRGHSHSVSTESSSFHSS 352
DB 301 LYAFLAGKFTSAQHATLSVRSGLKILSKRGHSHSVSTESSSFHSS 352

RESULT 8
US-09-104-063-4
Sequence 4, Application US/09104063
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,063
FILING DATE: 24-June-1998
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/701265
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664228
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-9530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-104-063-4

Query Match 100.0%; Score 1830; DB 15; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITSDNYTEEMSGDYSKKEPCFRENNANFNKIFLPTIYSITFLTGIVNGLYI 60
DB 1 MEGISITSDNYTEEMSGDYSKKEPCFRENNANFNKIFLPTIYSITFLTGIVNGLYI 60
QY 61 LVMGYOKKLSMTDKYRLHLSVADLLEFVITLPEWADVAVANWYGFNLCRAVHYTYVNL 120
DB 61 LVMGYOKKLSMTDKYRLHLSVADLLEFVITLPEWADVAVANWYGFNLCRAVHYTYVNL 120
QY 121 YSSVLLIAFSLDRIYLAIVHATNSQRPKLLAEKVYVYGVWIPALLTIPDFIFANVSEA 180
DB 121 YSSVLLIAFSLDRIYLAIVHATNSQRPKLLAEKVYVYGVWIPALLTIPDFIFANVSEA 180
QY 181 DDRYICDRFYNDLWVYVFOFOHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
DB 181 DDRYICDRFYNDLWVYVFOFOHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
QY 241 TVIIILAFACWLPYIYGISIDSFILLEIKOGCEFEVTYHKMISTEALAFHCCCLNPI 300
DB 241 TVIIILAFACWLPYIYGISIDSFILLEIKOGCEFEVTYHKMISTEALAFHCCCLNPI 300
QY 301 LYAFLAGKFTSAQHATLSVRSGLKILSKRGHSHSVSTESSSFHSS 352
DB 301 LYAFLAGKFTSAQHATLSVRSGLKILSKRGHSHSVSTESSSFHSS 352

RESULT 9
US-09-104-296-4
Sequence 4, Application US/09104296
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

```

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/104, 296
  FILING DATE: 24-June-1998
CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/701265
    FILING DATE: 22-AUG-1996
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/664228
    FILING DATE: 06-JUN-1996
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/076093
    FILING DATE: 11-JUN-1993
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 07/810782
    FILING DATE: 19-DEC-1991
  ATTORNEY/AGENT INFORMATION:
    NAME: Love, Richard B.
    REGISTRATION NUMBER: 34,659
  REFERENCE/DOCKET NUMBER: P0706P2C2
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415/225-5530
    TELEFAX: 415/952-9881
    TELEX: 910/371-7168
  INFORMATION FOR SEQ. ID NO: 4:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 352 amino acids
      TYPE: Amino Acid
      TOPOLOGY: Linear
US-09-104-296-4

```

```

Query Match      100.0%; Score 1830; DB 15; Length 352;
Best Local Similarity 100.0%; Pred. No. 2,1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITSDNTTEEMSGDYDSMKPCFREANANKIFLPTIYSIFLTGIVNGVLT 60
DB 1 MEGISITSDNTTEEMSGDYDSMKPCFREANANKIFLPTIYSIFLTGIVNGVLT 60
QY 61 LVNGYQKRLRMTDKYRLHLSVADLLFVITLPPWAVDAVANNYFGNFKCAHVITYNL 120
DB 61 LVNGYQKRLRMTDKYRLHLSVADLLFVITLPPWAVDAVANNYFGNFKCAHVITYNL 120
QY 121 YSSVLLAFISLDRYLAIVHATNSQRPRLAEKVVYGVWIPALLITPDIFFANVSEA 180
DB 121 YSSVLLAFISLDRYLAIVHATNSQRPRLAEKVVYGVWIPALLITPDIFFANVSEA 180
QY 181 DRYICDRFPNDLWVWFQFOHIMVGLIPGIVILSCYCIISKLSHSGHOKRKALKT 240
DB 181 DRYICDRFPNDLWVWFQFOHIMVGLIPGIVILSCYCIISKLSHSGHOKRKALKT 240
QY 241 TVILLAFACWLPYYIGISIDSFILLEIIKOGCEFEENTVHKWISITELAFHCCLNPI 300
DB 241 TVILLAFACWLPYYIGISIDSFILLEIIKOGCEFEENTVHKWISITELAFHCCLNPI 300
QY 301 LYAFGAKFKTSAQHALLTSVSRGSSSLKILSKRGHSSSVSTESSSPHSS 352
DB 301 LYAFGAKFKTSAQHALLTSVSRGSSSLKILSKRGHSSSVSTESSSPHSS 352

```

```

RESULT 10
US-09-122-068-2
: Sequence 2, Application US/09122068
: GENERAL INFORMATION:
: APPLICANT: PILLARISSETTI, KODANDARAM
: APPLICANT: GUPTA, SHALLEY
: TITLE OF INVENTION: CXCR4B: A HUMAN SPLICE VARIANT
: TITLE OF INVENTION: OF CXCR4 CHEMOKINE RECEPTOR

```

```

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/122, 068
  FILING DATE:
CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 60/056,601
    FILING DATE: 20-AUG-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Prestia, Paul F.
    REGISTRATION NUMBER: 23,031
    REFERENCE/DOCKET NUMBER: GH-70229
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 610-407-0700
    TELEFAX: 610-407-0701
    TELEX: 846169
  INFORMATION FOR SEQ. ID NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 356 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: Linear
      MOLECULE TYPE: protein
US-09-122-068-2

```

```

Query Match      98.8%; Score 1808; DB 15; Length 356;
Best Local Similarity 99.4%; Pred. No. 2,7e-165;
Matches 347; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ISITSDNTTEEMSGDYDSMKPCFREANANKIFLPTIYSIFLTGIVNGVLT 63
DB 8 LQITSDNTTEEMSGDYDSMKPCFREANANKIFLPTIYSIFLTGIVNGVLT 67
QY 64 GYQKRLRMTDKYRLHLSVADLLFVITLPPWAVDAVANNYFGNFKCAHVITYNL 123
DB 68 GYQKRLRMTDKYRLHLSVADLLFVITLPPWAVDAVANNYFGNFKCAHVITYNL 127
QY 124 VLLAFISLDRYLAIVHATNSQRPRLAEKVVYGVWIPALLITPDIFFANVSEADR 183
DB 128 VLLAFISLDRYLAIVHATNSQRPRLAEKVVYGVWIPALLITPDIFFANVSEADR 187
QY 184 YICDRFPNDLWVWFQFOHIMVGLIPGIVILSCYCIISKLSHSGHOKRKALTTYI 243
DB 188 YICDRFPNDLWVWFQFOHIMVGLIPGIVILSCYCIISKLSHSGHOKRKALTTYI 247
QY 244 LILAFACWLPYYIGISIDSFILLEIIKOGCEFEENTVHKWISITELAFHCCLNPI 303
DB 248 LILAFACWLPYYIGISIDSFILLEIIKOGCEFEENTVHKWISITELAFHCCLNPI 307
QY 304 FLGAKFKTSAQHALLTSVSRGSSSLKILSKRGHSSSVSTESSSPHSS 352
DB 308 FLGAKFKTSAQHALLTSVSRGSSSLKILSKRGHSSSVSTESSSPHSS 356

```

```

RESULT 11
US-08-182-962-6
: Sequence 6, Application US/08182962
: GENERAL INFORMATION:
: APPLICANT: Charo, Israel
: APPLICANT: Coughlin, Shaun

```

TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Goddard Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UOAL-237/OLUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-446-669-6

Query Match	Best Local Similarity	97.8%	Score 1789	DB 7	Length 352
Matches 346	Conservative	0	Mismatches 6	Indels	Gaps
QY	1	MEGISIYTSDMYTEEMSGSDYDSMKPEPCFREANANFNKIFLPTIYSIFLTGIVGNGLVI	60		
Db	1	MEGISIYTSDMYTEEMSGSDYDSMKPEPCFREANANFNKIFLPTIYSIFLTGIVGNGLVI	60		
QY	61	LYMGYOKKLREMEPKYRRLHLSVADLLFPTTLPANAVADVAMWYSGNFIKCAVHYTYTNL	120		
Db	61	LYMGYOKKLRSMTQKRYRLHLSVADLLFPTTLPANAVADVAMWYSGNFIKCAVHYTYTNL	120		
QY	121	YSSVLLIAFLISLDYRLAIVHATNSQRPRLKLAERYVYGVNIPALLLTIIPDFIFANVSEA	180		
Db	121	YSSVLLIAFLISLDYRLAIVHATNSQRPRLKLAERYVYGVNIPALLLTIIPDFIFANVSEA	180		
QY	181	DDRYICDREYENDLMVWYVFOFOHIMVGLILPGIYILSCYCIISKLSSHOKHOKALKT	240		
Db	181	DDRYICDREYENDLMVWYVFOFOHIMVGLILPGIYILSCYCIISKLSSHOKHOKALKT	240		
QY	241	TVLLILFAFACMLPYIYIGISIDSEFLLEIIKQGEFENTVHKWISTEALAFPHCCLPDI	300		
Db	241	TVLLILFAFACMLPYIYIGISIDSEFLLEIIKQGEFENTVHKWISTEALAFPHCCLPDI	300		
QY	301	LYAFILGAKFKTSAOHALTSVSRGSSILKLSGKRGHGSVSTEESSESHS	352		
Db	301	LYAFILGAKFKTSAOHALTSVSRGSSILKLSGKRGHGSVSTEESSESHS	352		

RESULT 13

US-08-450-393-6

Sequence 6, Application US/08450393

GENERAL INFORMATION:

APPLICANT: Chato, Israel

TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

TITLE OF INVENTION: PROTEIN RECEPTORS

NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Goddard Castro Huddleson & Tatum
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94306-2155
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,393
 FILING DATE: May 25, 1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Cseert, Luan
 REGISTRATION NUMBER: 31,822
 REFERENCE/DOCKET NUMBER: UCAL-237/020US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5165
 TELEFAX: 415-8857-0663
 TELEX: 380816COOLEYPA
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 US-08-450-393-6

Query Match 97.8%; Score 1789; DB 7; Length 352;
 Best Local Similarity 98.3%; Pred. No. 1.8e-163;
 Matches 346; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	1	MEGIYTSNDYTEMGSGDYDMSKPECFREANFNKIFLPTIYSIFLTGIVNGGLVI	60
DB	1	MEGIITYSDNTEMGSDYDMSKPECFREANFNKIFLPTIYSIFLTGIVNGGLVI	60
QY	61	LVMGYQKLRSTDKYRLHLVADLLFVITLPEFMAVDAAVMYFGNFKCAVHYITVNL	120
DB	61	LVMGYQKLRSTDKYRLHLVADLLFVITLPEFMAVDAAVMYFGNFKCAVHYITVNL	120
QY	121	YSSVLIAFISLDRIYLAIVHATNSQPRKILAEKVYVGVWIPALLITPDIIFANVSEA	180
DB	121	YSSVLIAFISLDRIYLAIVHATNSQPRKILAEKVYVGVWIPALLITPDIIFANVSEA	180
QY	181	DDRYICDREYPNDLVVVFQFHIMVGLIPGIVILSCYCIISKLSHSGHQRRAALMT	240
DB	181	DDRYICDREYPNDLVVVFQFHIMVGLIPGIVILSCYCIISKLSHSGHQRRAALMT	240
QY	241	YVILILAFACWLPYIIGISIDSFILLETIKQCEFEIVHKWISTEALAFHCLNPI	300
DB	241	YVILILAFACWLPYIIGISIDSFILLETIKQCEFEIVHKWISTEALAFHCLNPI	300
QY	301	LVAFGLAKFKTSQHALTSVSRGSSILSKGRGSHSVSTESSESSFHSS	352
DB	301	LVAFGLAKFKTSQHALTSVSRGSSILSKGRGSHSVSTESSESSFHSS	352

RESULT 14
 US-07-977-452A-21
 Sequence 21, Application US/0797452A
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schwaikart, Vicki L.
 TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Bicknell
 STREET: Two First National Plaza, Suite 2100
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/977,452A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Noland, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 30928
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 346-5750
 TELEFAX: (312) 984-9740
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 337 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-977-452A-21

Query Match 95.7%; Score 1752; DB 2; Length 337;
 Best Local Similarity 100.0%; Pred. No. 5.9e-160;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	16	MGSGDYDMSKPECFREANFNKIFLPTIYSIFLTGIVNGGLVILVGYQKLRSMYDK	75
DB	1	MGSGDYDMSKPECFREANFNKIFLPTIYSIFLTGIVNGGLVILVGYQKLRSMYDK	60
QY	76	YRLHLVADLLFVITLPEFMAVDAAVMYFGNFKCAVHYITVNLVSSVLIATISDRY	135
DB	61	YRLHLVADLLFVITLPEFMAVDAAVMYFGNFKCAVHYITVNLVSSVLIATISDRY	120
QY	136	LAIVHATNSQPRKILAEKVYVGVWIPALLITPDIIFANVSEADRYICDREYPNDLV	195
DB	121	LAIVHATNSQPRKILAEKVYVGVWIPALLITPDIIFANVSEADRYICDREYPNDLV	180
QY	196	VVVFQFHIMVGLIPGIVILSCYCIISKLSHSGHQRRAALMTVILILAFACWLPY	255
DB	181	VVVFQFHIMVGLIPGIVILSCYCIISKLSHSGHQRRAALMTVILILAFACWLPY	240
QY	256	YIGISIDSFILLETIKQCEFEIVHKWISTEALAFHCLNPIVAFGLAKFKTSQH	315
DB	241	YIGISIDSFILLETIKQCEFEIVHKWISTEALAFHCLNPIVAFGLAKFKTSQH	300
QY	316	ALTSVSRGSSILSKGRGSHSVSTESSESSFHSS	352
DB	301	ALTSVSRGSSILSKGRGSHSVSTESSESSFHSS	337

RESULT 15
 US-08-245-242-46
 Sequence 46, Application US/08245242
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schwaikart, Vicki L.
 TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:


```

: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/245,242
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/153,848
: FILING DATE: 17-NOV-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/977,452
: FILING DATE: 17-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Noland, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31794
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
:
: INFORMATION FOR SEQ ID NO: 46:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 337 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-245-242-46

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```

Query Match          95.7%; Score 1752; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 5.9e-160;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MGSQDYDSMKPCFRENANFNKIFLPTIYSIIFLTGIVGNGLYLVWGYOKLRSMTDK 75
   |||||||
Db 1 MGSQDYDSMKPCFRENANFNKIFLPTIYSIIFLTGIVGNGLYLVWGYOKLRSMTDK 60
   |||||||

QY 76 YRLHLSYADLLFVITLFPMAVDVANNYFGNFLCKAVHVIYTVNLSSVLLIAFISLDY 135
   |||||||
Db 61 YRLHLSYADLLFVITLFPMAVDVANNYFGNFLCKAVHVIYTVNLSSVLLIAFISLDY 120
   |||||||

QY 136 LAIVHATNSORPRKLLAEKVVYGVWIPALLITIPDFIFANVSEADDRYICDRFPNDLW 195
   |||||||
Db 121 LAIVHATNSORPRKLLAEKVVYGVWIPALLITIPDFIFANVSEADDRYICDRFPNDLW 180
   |||||||

QY 196 VVVFQFHIMWGLIPGIVILSCYCIISKLSHSGHQKRAKLTIVILLIAFFACWLPY 255
   |||||||
Db 181 VVVFQFHIMWGLIPGIVILSCYCIISKLSHSGHQKRAKLTIVILLIAFFACWLPY 240
   |||||||

QY 256 YIGISIDSFILLEIKOGCEFEENTVHKWISTEALAFPHCCCLNPILYAFUGAKFTSAOH 315
   |||||||
Db 241 YIGISIDSFILLEIKOGCEFEENTVHKWISTEALAFPHCCCLNPILYAFUGAKFTSAOH 300
   |||||||

QY 316 ALTSVSRGSSSLKILSKGRGSHSVSTESSESSPHSS 352
   |||||||
Db 301 ALTSVSRGSSSLKILSKGRGSHSVSTESSESSPHSS 337

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 14, 1999, 09:50:15 : Search time 10.08 Seconds
(without alignments)
344.610 Million cell updates/sec

Title: US-09-104-063-4
Perfect score: 1830
Sequence: 1 MEGISITSDNYTEEMSGSD.....KRGHSSVSTRESSSPHSS 352

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database : Issued Patents-AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/PCTUS9.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1830	100.0	352	1	US-08-202-056-3	Sequence 3, Appl1
2	1830	100.0	352	1	US-08-076-093A-4	Sequence 4, Appl1
3	1830	100.0	352	2	US-08-701-265-4	Sequence 4, Appl1
4	1830	100.0	352	2	US-08-284-586-4	Sequence 4, Appl1
5	1830	100.0	352	2	US-08-805-478-4	Sequence 4, Appl1
6	1789	97.8	352	1	US-08-450-393A-6	Sequence 6, Appl1
7	1789	97.8	352	3	PCT-US95-00476-6	Sequence 6, Appl1
8	1752	95.7	337	2	US-08-153-848-46	Sequence 6, Appl1
9	1752	95.7	337	2	PCT-US93-11153-46	Sequence 46, Appl1
10	568	31.0	355	1	US-07-759-568-1	Sequence 1, Appl1
11	568	31.0	355	1	US-08-202-056-7	Sequence 7, Appl1
12	568	31.0	355	1	US-08-450-393A-8	Sequence 8, Appl1
13	568	31.0	355	3	PCT-US95-00476-8	Sequence 8, Appl1
14	557.5	30.5	350	1	US-08-202-056-1	Sequence 1, Appl1
15	557.5	30.5	350	1	US-08-076-093A-2	Sequence 2, Appl1
16	557.5	30.5	350	1	US-08-450-393A-7	Sequence 7, Appl1
17	557.5	30.5	350	2	US-08-410-453A-1	Sequence 1, Appl1
18	557.5	30.5	350	2	US-08-701-265-2	Sequence 2, Appl1
19	557.5	30.5	350	2	US-08-410-454A-1	Sequence 1, Appl1
20	557.5	30.5	350	2	US-08-284-586-2	Sequence 2, Appl1
21	557.5	30.5	350	2	US-08-410-456A-1	Sequence 1, Appl1
22	557.5	30.5	350	2	US-08-805-478-2	Sequence 2, Appl1
23	557.5	30.5	350	2	PCT-US95-00476-7	Sequence 7, Appl1
24	557.5	30.4	378	2	US-08-153-848-7	Sequence 7, Appl1
25	557.5	30.4	378	2	US-08-153-848-15	Sequence 15, Appl1
26	557.5	30.4	378	2	US-08-153-848-19	Sequence 19, Appl1
27	557.5	30.4	410	3	PCT-US93-11153-7	Sequence 7, Appl1
28	557.5	30.4	378	3	PCT-US93-11153-15	Sequence 15, Appl1
29	557.5	30.4	359	2	PCT-US93-11153-19	Sequence 19, Appl1
30	550	30.1	359	2	US-08-153-848-24	Sequence 24, Appl1
31	550	30.1	359	2	PCT-US93-11153-24	Sequence 24, Appl1
32	549.5	30.0	355	2	US-08-153-848-28	Sequence 28, Appl1
33	549.5	30.0	355	2	US-08-153-848-32	Sequence 32, Appl1
34	549.5	30.0	355	3	PCT-US93-11153-28	Sequence 28, Appl1
35	549.5	30.0	355	3	PCT-US93-11153-32	Sequence 32, Appl1
36	540	29.5	372	1	US-08-202-056-5	Sequence 5, Appl1
37	540	29.5	372	1	US-08-076-093A-6	Sequence 6, Appl1
38	540	29.5	372	1	US-08-701-265-6	Sequence 6, Appl1
39	540	29.5	372	2	US-08-284-586-6	Sequence 6, Appl1

40	540	29.5	372	2	US-08-805-478-6	Sequence 6, Appl1
41	538	29.4	378	1	US-08-383-750-2	Sequence 2, Appl1
42	538	29.4	378	2	US-08-383-751A-2	Sequence 2, Appl1
43	538	29.4	378	3	PCT-US93-09636-2	Sequence 2, Appl1
44	528	28.9	374	1	US-08-450-393A-2	Sequence 2, Appl1
45	528	28.9	374	3	PCT-US95-00476-2	Sequence 2, Appl1

ALIGNMENTS

```
RESULT 1
US-08-202-056-3
: Sequence 3, Application US/08202056
: Patent No. 5440021
: GENERAL INFORMATION:
: APPLICANT: Chuntcharapai, Anan
: APPLICANT: Hebert, Caroline
: APPLICANT: Kim, Kyung Jin
: APPLICANT: Lee, James
: TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/202,056
: FILING DATE: 25-FEB-1994
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/677211
: FILING DATE: 29-MAR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: 706P3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 352 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08-202-056-3

Query Match      100.0%; Score 1830; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6,4e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEGISITSDNYTEEMSGSDYDKKEPCFDEENANFKIFLPTYSITFTGIYGNGLVI 60
1 MEGISITSDNYTEEMSGSDYDKKEPCFDEENANFKIFLPTYSITFTGIYGNGLVI 60
61 LVMGYQKRLSMYDKYRLHLSVADLFTVTLPEWAVDAVANWYFGNFLCAVHYITVNL 120
61 LVMGYQKRLSMYDKYRLHLSVADLFTVTLPEWAVDAVANWYFGNFLCAVHYITVNL 120
61 LVMGYQKRLSMYDKYRLHLSVADLFTVTLPEWAVDAVANWYFGNFLCAVHYITVNL 120
121 YSSVLLIAFISLDYRLAIVAHATNSORPRKLLAEKVYVGVWIPALLITIDPFIANVSEA 180
121 YSSVLLIAFISLDYRLAIVAHATNSORPRKLLAEKVYVGVWIPALLITIDPFIANVSEA 180

QY 181 DRRYICDRFYNDLWVVFQFQHMVGLIPGIVILSCYIIISKLSHSGHQRKALKT 240
| | | | |
Db 181 DRRYICDRFYNDLWVVFQFQHMVGLIPGIVILSCYIIISKLSHSGHQRKALKT 240
QY 241 TVLIIAFAFCWLPYYIGISIDSFILLEITIKGCEFEENTYHKWISTEALAFHCCLNPI 300
| | | | |
Db 241 TVLIIAFAFCWLPYYIGISIDSFILLEITIKGCEFEENTYHKWISTEALAFHCCLNPI 300
QY 301 LVAFIAGKFTSAQHALTSVSRGSSLKILSKGRGSHSVSTESESSSFHSS 352
| | | | |
Db 301 LVAFIAGKFTSAQHALTSVSRGSSLKILSKGRGSHSVSTESESSSFHSS 352

RESULT 2
US-08-076-093A-4
; Sequence 4, Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-076-093A-4

Query Match 100.0%; Score 1830; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITDNTTEEMSGSDYDSMKPECFREANANFKIFLPTIYSIIFLTGIVNGGLVI 60
| | | | |
Db 1 MEGISITDNTTEEMSGSDYDSMKPECFREANANFKIFLPTIYSIIFLTGIVNGGLVI 60
QY 61 LVNGYOKRLSRMTDKYRLHLISVADLLFVITLFPWAVDAVANMTFGNFCACAVIYITVNL 120
| | | | |
Db 61 LVNGYOKRLSRMTDKYRLHLISVADLLFVITLFPWAVDAVANMTFGNFCACAVIYITVNL 120

QY 121 YSVLLIAFISIDRYIAIYHATNSORPRKILAEKVYVGVWIPALLTIPDFIFANVSEA 180
| | | | |
Db 121 YSVLLIAFISIDRYIAIYHATNSORPRKILAEKVYVGVWIPALLTIPDFIFANVSEA 180
QY 181 DRRYICDRFYNDLWVVFQFQHMVGLIPGIVILSCYIIISKLSHSGHQRKALKT 240
| | | | |
Db 181 DRRYICDRFYNDLWVVFQFQHMVGLIPGIVILSCYIIISKLSHSGHQRKALKT 240
QY 241 TVLIIAFAFCWLPYYIGISIDSFILLEITIKGCEFEENTYHKWISTEALAFHCCLNPI 300
| | | | |
Db 241 TVLIIAFAFCWLPYYIGISIDSFILLEITIKGCEFEENTYHKWISTEALAFHCCLNPI 300
QY 301 LVAFIAGKFTSAQHALTSVSRGSSLKILSKGRGSHSVSTESESSSFHSS 352
| | | | |
Db 301 LVAFIAGKFTSAQHALTSVSRGSSLKILSKGRGSHSVSTESESSSFHSS 352

RESULT 3
US-08-701-265-4
; Sequence 4, Application US/08701265
; Patent No. 576457
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,265
; FILING DATE: 22-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-701-265-4

Query Match 100.0%; Score 1830; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MEGISITSDNTEEMSGSDYDSMKPCPCRENNANFKIFLPTIYSIFLGIINGGLVI 60
    |||||||
Db 1 MEGISITSDNTEEMSGSDYDSMKPCPCRENNANFKIFLPTIYSIFLGIINGGLVI 60
OY 61 LVMGYOKRLSRMTDKYRLHLVSADLLFVITLPEFMAVDAAVMYFQNFCKAHVITYNL 120
    |||||||
Db 61 LVMGYOKRLSRMTDKYRLHLVSADLLFVITLPEFMAVDAAVMYFQNFCKAHVITYNL 120
OY 121 YSSVILAFISIDRLAIVHATNSORPRKLLAEKVVYGVWIPALLLTPDIFANVSEA 180
    |||||||
Db 121 YSSVILAFISIDRLAIVHATNSORPRKLLAEKVVYGVWIPALLLTPDIFANVSEA 180
OY 181 DDRYICDRFPNDLMWVVFQFQHIWGLILPGIYILSCYCIITISKLSHGOKRKALKT 240
    |||||||
Db 181 DDRYICDRFPNDLMWVVFQFQHIWGLILPGIYILSCYCIITISKLSHGOKRKALKT 240
OY 241 TVIILAFACWLPYYIGISIDSFILLETIKOGCEFEVTHKWSITELAFHCCLNPI 300
    |||||||
Db 241 TVIILAFACWLPYYIGISIDSFILLETIKOGCEFEVTHKWSITELAFHCCLNPI 300
OY 301 LYAFIGAFTSAQHATLSVSRGSSSLKILSKGRGHSVSTESSSSFHSS 352
    |||||||
Db 301 LYAFIGAFTSAQHATLSVSRGSSSLKILSKGRGHSVSTESSSSFHSS 352
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RESULT 4

US-08-284-586-4

```
Sequence 4, Application US/08284586
Patent No. 5840856
GENERAL INFORMATION:
APPLICANT: Chuntharapal, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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US-08-284-586-4

Query Match 100.0%; Score 1830; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 6, 4e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MEGISITSDNTEEMSGSDYDSMKPCPCRENNANFKIFLPTIYSIFLGIINGGLVI 60
    |||||||
Db 1 MEGISITSDNTEEMSGSDYDSMKPCPCRENNANFKIFLPTIYSIFLGIINGGLVI 60
OY 61 LVMGYOKRLSRMTDKYRLHLVSADLLFVITLPEFMAVDAAVMYFQNFCKAHVITYNL 120
    |||||||
Db 61 LVMGYOKRLSRMTDKYRLHLVSADLLFVITLPEFMAVDAAVMYFQNFCKAHVITYNL 120
OY 121 YSSVILAFISIDRLAIVHATNSORPRKLLAEKVVYGVWIPALLLTPDIFANVSEA 180
    |||||||
Db 121 YSSVILAFISIDRLAIVHATNSORPRKLLAEKVVYGVWIPALLLTPDIFANVSEA 180
OY 181 DDRYICDRFPNDLMWVVFQFQHIWGLILPGIYILSCYCIITISKLSHGOKRKALKT 240
    |||||||
Db 181 DDRYICDRFPNDLMWVVFQFQHIWGLILPGIYILSCYCIITISKLSHGOKRKALKT 240
OY 241 TVIILAFACWLPYYIGISIDSFILLETIKOGCEFEVTHKWSITELAFHCCLNPI 300
    |||||||
Db 241 TVIILAFACWLPYYIGISIDSFILLETIKOGCEFEVTHKWSITELAFHCCLNPI 300
OY 301 LYAFIGAFTSAQHATLSVSRGSSSLKILSKGRGHSVSTESSSSFHSS 352
    |||||||
Db 301 LYAFIGAFTSAQHATLSVSRGSSSLKILSKGRGHSVSTESSSSFHSS 352
```

RESULT 5

US-08-805-478-4

```
Sequence 4, Application US/08805478
Patent No. 5874543
GENERAL INFORMATION:
APPLICANT: Chuntharapal, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1C1
TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-805-478-4

Query Match 100.0%; Score 1830; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITSDNTYEMSGSDYDSMKPCFRENANFNKIFLPTIYSIFLGTGNGLVI 60
DB 1 MEGISITSDNTYEMSGSDYDSMKPCFRENANFNKIFLPTIYSIFLGTGNGLVI 60
QY 61 LVNGYQKRLSMTDKYRLHLVADLLEFVITLPEWAVDAVANNYFGNPLCKAVHYITVNL 120
DB 61 LVNGYQKRLSMTDKYRLHLVADLLEFVITLPEWAVDAVANNYFGNPLCKAVHYITVNL 120
QY 121 YSSVLLIAFISLDRLAIYHATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEA 180
DB 121 YSSVLLIAFISLDRLAIYHATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEA 180
QY 181 DDRICDRFPNDLVVYVFOFQHMVGLLPGVILISCYCIISKLSHSGHQKRAKLT 240
DB 181 DDRICDRFPNDLVVYVFOFQHMVGLLPGVILISCYCIISKLSHSGHQKRAKLT 240
QY 241 TVILILAFACWLPYYIGISIDSFILLEITIKGCEPENTVHKWISTEALAFHCCLNPI 300
DB 241 TVILILAFACWLPYYIGISIDSFILLEITIKGCEPENTVHKWISTEALAFHCCLNPI 300
QY 301 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGSHSVSTESSSSPHSS 352
DB 301 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGSHSVSTESSSSPHSS 352

RESULT 6
US-08-450-393A-6
Sequence 6, Application US/08450393A
Patent No. 5707815

GENERAL INFORMATION:
APPLICANT: Charo, Israel
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cseert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/020US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663

TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-450-393A-6

Query Match 97.8%; Score 1789; DB 1; Length 352;
Best Local Similarity 98.3%; Pred. No. 1.5e-140;
Matches 346; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MEGISITSDNTYEMSGSDYDSMKPCFRENANFNKIFLPTIYSIFLGTGNGLVI 60
DB 1 MEGISITSDNTYEMSGSDYDSMKPCFRENANFNKIFLPTIYSIFLGTGNGLVI 60
QY 61 LVNGYQKRLSMTDKYRLHLVADLLEFVITLPEWAVDAVANNYFGNPLCKAVHYITVNL 120
DB 61 LVNGYQKRLSMTDKYRLHLVADLLEFVITLPEWAVDAVANNYFGNPLCKAVHYITVNL 120
QY 121 YSSVLLIAFISLDRLAIYHATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEA 180
DB 121 YSSVLLIAFISLDRLAIYHATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEA 180
QY 181 DDRICDRFPNDLVVYVFOFQHMVGLLPGVILISCYCIISKLSHSGHQKRAKLT 240
DB 181 DDRICDRFPNDLVVYVFOFQHMVGLLPGVILISCYCIISKLSHSGHQKRAKLT 240
QY 241 TVILILAFACWLPYYIGISIDSFILLEITIKGCEPENTVHKWISTEALAFHCCLNPI 300
DB 241 TVILILAFACWLPYYIGISIDSFILLEITIKGCEPENTVHKWISTEALAFHCCLNPI 300
QY 301 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGSHSVSTESSSSPHSS 352
DB 301 LVAFLEAKFKTSQAHALTSVSRGSSSLKILSKGRGSHSVSTESSSSPHSS 352

RESULT 7
PCT-US95-00476-6
Sequence 6, Application PC/TUS9500476
GENERAL INFORMATION:

APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEITICAL: NO
PCT-US95-00476-6

Query Match 97.8%; Score 1789; DB 3; Length 352;
Best Local Similarity 98.3%; Pred. No. 1.5e-140;
Matches 346; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MEGSITSDNYTEEMSGDYDSKPECFRENNANFNKIFLPTIYSIFLTGIVGNGLYI 60
DB 1 MEGSITSDNYTEEMSGDYDSKPECFRENNANFNKIFLPTIYSIFLTGIVGNGLYI 60
QY 61 LVMGYQKRLRMTDKYRLHLVSADLLFVITLPFAVDAVANMFNGFLCKAVHYITVNL 120
DB 61 LVMGYQKRLRMTDKYRLHLVSADLLFVITLPFAVDAVANMFNGFLCKAVHYITVNL 120
QY 121 YSSVLLIAFLISLDRIYLAIVHATNSQRPRLAEKVYVGVWIPALLTIPDFIFANVSEA 180
DB 121 YSSVLLIAFLISLDRIYLAIVHATNSQRPRLAEKVYVGVWIPALLTIPDFIFANVSEA 180
QY 181 DDRIYCDREFYNDLMVVFQFOHIMVGLIPGIVILSCYIIISKLSHSGHOKRAKLT 240
DB 181 DDRIYCDREFYNDLMVVFQFOHIMVGLIPGIVILSCYIIISKLSHSGHOKRAKLT 240
QY 241 TVLILAFACMLPYIYIGISIDSFILLEIKQGEFENTVHKWISTEALAFPHCCLNPI 300
DB 241 TVLILAFACMLPYIYIGISIDSFILLEIKQGEFENTVHKWISTEALAFPHCCLNPI 300
QY 301 LYALGAKFTSAQHALTSVSRGSSLKILSKGRGHSVSTESSESSFHSS 352
DB 301 LYALGAKFTSAQHALTSVSRGSSLKILSKGRGHSVSTESSESSFHSS 352

RESULT 8
US-08-153-848-46

Sequence 46, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-46

Query Match 95.7%; Score 1752; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.6e-137;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MGSQDYDSMKPECFRENNANFNKIFLPTIYSIFLTGIVGNGLYLVMGYQKRLRMTDK 75
DB 1 MGSQDYDSMKPECFRENNANFNKIFLPTIYSIFLTGIVGNGLYLVMGYQKRLRMTDK 75
QY 76 YRLHLVSADLLFVITLPFAVDAVANMFNGFLCKAVHYITVNLSSVLLIAFLISLDY 135
DB 76 YRLHLVSADLLFVITLPFAVDAVANMFNGFLCKAVHYITVNLSSVLLIAFLISLDY 135
QY 136 LAIVHATNSQRPRLAEKVYVGVWIPALLTIPDFIFANVSADDRYICDREYNDLM 195
DB 136 LAIVHATNSQRPRLAEKVYVGVWIPALLTIPDFIFANVSADDRYICDREYNDLM 195
QY 196 VVVFQFOHIMVGLIPGIVILSCYIIISKLSHSGHOKRAKLTYYLILAFACMLPY 255
DB 196 VVVFQFOHIMVGLIPGIVILSCYIIISKLSHSGHOKRAKLTYYLILAFACMLPY 255
QY 256 YIGISIDSFILLEIKQGEFENTVHKWISTEALAFPHCCLNPIYALGAKFTSAQH 315
DB 256 YIGISIDSFILLEIKQGEFENTVHKWISTEALAFPHCCLNPIYALGAKFTSAQH 315
QY 316 ALTSVSRGSSLKILSKGRGHSVSTESSESSFHSS 352
DB 316 ALTSVSRGSSLKILSKGRGHSVSTESSESSFHSS 352

RESULT 9

PCT-US93-11153-46
Sequence 46, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-46

Query Match 95.7%; Score 1752; DB 3; Length 337;
Best Local Similarity 100.0%; Pred. No. 1,6e-137; Mismatches 0; Indels 0; Gaps 0;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MGSQDYDSMKKEPCFRENNANFNKIFLPTIYSIIIFLTGIVNGVLIVMGYQKRLSMTDK 75
DB 1 MGSQDYDSMKKEPCFRENNANFNKIFLPTIYSIIIFLTGIVNGVLIVMGYQKRLSMTDK 60
QY 76 YRLHLSVADLLFVITLPPFAVDVANWYFGNFLCKAVHYITVNVIXSSVLLIAFTSLDRY 135
DB 61 YRLHLSVADLLFVITLPPFAVDVANWYFGNFLCKAVHYITVNVIXSSVLLIAFTSLDRY 120
QY 136 LAIVHATNSQRPRLKLAERKVVYGVWIPALLLTIPDFIFANVSEADDRICDRFPNDLM 195
DB 121 LAIVHATNSQRPRLKLAERKVVYGVWIPALLLTIPDFIFANVSEADDRICDRFPNDLM 180
QY 196 VVVFQFHIMVGLIPGIVILSCYIIISKLSHSGHOKRKALKTTVILLIAFACWLPY 255
DB 181 VVVFQFHIMVGLIPGIVILSCYIIISKLSHSGHOKRKALKTTVILLIAFACWLPY 240
QY 256 YIGISIDFILLEITKOCCEPENTVHKMISTREALAFHCCNPLIYAFKAKETSQNH 315
DB 241 YIGISIDFILLEITKOCCEPENTVHKMISTREALAFHCCNPLIYAFKAKETSQNH 300
QY 316 ALTSVRSGLSKLSKGRGHSVSTSESSSFHSS 352
DB 301 ALTSVRSGLSKLSKGRGHSVSTSESSSFHSS 337

RESULT 10
US-07-759-568-1
Sequence 1, Application US/07759568
Patent No. 5374506
GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman, Darby & Cushman
STREET: 1615 L Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/759, 568
FILING DATE: 19910913
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-759-568-1

Query Match 31.0%; Score 568; DB 1; Length 355;
Best Local Similarity 35.3%; Pred. No. 6,7e-40; Mismatches 119; Indels 54; Gaps 11;
Matches 132; Conservative 69; Mismatches 119; Indels 54; Gaps 11;

QY 9 SDNYT-----EMSGDYDSM-----KEPCFRENNANFNKIFLPTIYSIIIFLTGIVN 56
DB 3 SDSFEDFMKGBDLSNYSYSTLPFLDAPC-EPESLEINKYFVITVIALVFLSLGN 61
QY 57 GLVITVMGYQKRLSMTDKYRLHLSVADLLFVITLPPFAVDVANWYFGNFLCKAVHYIY 116
DB 62 SLVMLVILYSVGRSVYDVLLNLADLLPALTLPIAASKVGVWIFGTFELCVSDLK 121
QY 117 TVNLYSSVLLIAFTSLDRYLAIVHATNSQRPRLKLAERKVVYGVWIPALLLTIPDFI-- 175
DB 122 EVNFISSGILLACISVDKRLIVHATRLITQKRLV-KFICLSIWGSLALAVLLFRR 180
QY 175 ----ANVSEADDRICDRFPNDL--VVVFQFHIMVGLIPGIVILSCYIIISKLSH 228
DB 181 TVYSSNVSPA-----CYEDMGNTANWRLRLILPQSFGEIVPLILMLFCGFLRTLFK 235
QY 229 SKHQKRAKLTYYILLIAFACWLPYIIGISIDFILLEITKOCCEPENTVHKMISTE 288
DB 236 AHMGCKHAKMVIYAVVILFLLCWPYNLVLLADTLMTQVIOETCERRNIDALDATE 295
QY 289 ALAFHCCNPLIYAFKAKETSQNHATSVSRSGLSKLSKGRGHSVSTSESSSFHSS 345
DB 296 ILGILHSCNPLIYAFIQKRR-----HCL-----LKILAI-----HGLISDSLPKD 338
QY 345 -----ESSSFHSS 352
DB 339 SRPSFVGSSSGHTS 352

RESULT 11
US-08-202-056-7
Sequence 7, Application US/08202056
Patent No. 5440021
GENERAL INFORMATION:
APPLICANT: Chuntcharapai, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202, 056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berlin, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
PCT-US95-00476-8

Query Match 31.0%; Score 568; DB 3; Length 355;
Best Local Similarity 35.3%; Pred. No. 6,7e-40;
Matches 132; Conservative 69; Mismatches 119; Indels 54; Gaps 11;

QY 9 SDNYT-----EEMSGDYDSM-----KEPCFREMANFNKIPLTIYSIIFTLGIYGN 56
DB 3 SDSFEDFKMGEDLSNYSYSTLPPLLDAPC-EPESLEINKYFVYIYALVFLSLGN 61
QY 57 GIVILVMGYOKRLBSMTQKRYRLHSVADLFTLPEFNAVDAVAMVYGNFCKAVHYIY 116
DB 62 SLVMIYILSRGRSVTDVYLLNLADLFLALTPIMASKVNGWIGTFCKVSLK 121
QY 117 TVNLSSVLIILAFISLDRLAIVHATNSQRPRLAEKVYVGVNIPALLTIIPDFIF-- 175
DB 122 EVNEFSGLILLACISVDRLAIVHATRLITQKRYLV-KFICISINGSLILLAPVLLPR 180
QY 175 ----ANSEADDRYICDRFPNDL--WVVFQOHIMGLIPGIYILSCYIIISKLSH 228
DB 181 TVYSSNVSPA-----CYEDMGNNNTANMRLRLIPQSEGFIVPLIMFCYGFLLTLEK 235
QY 229 SKGHOKRKALKTTVILLAFACWLPYIGISIDSEFILLEIKOGCEFEFNTVHKMISTE 288
DB 236 AHMGOKHRAMRYIAVLFELCMPLYNLVLLADTLMRTQVIOETCERRNHIDRALDATE 295
QY 289 ALAFPHCLNPIILYAFLGAKFKTSQHAULTSVRSGLKILSKGRGSHSVSTES---- 345
DB 296 ILGIHSCNLPILYAFIQGKFR---HGL-----LKIILAI-----HGLISKSLPRD 338
QY 345 -----ESSPHSS 352
DB 339 SRPFSVCGSSGHTS 352

RESULT 14
US-08-202-056-1
Sequence 1, Application US/08202056
Patent No. 5440021
GENERAL INFORMATION:
APPLICANT: Chuntharapal, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-202-056-1

Query Match 30.5%; Score 557.5; DB 1; Length 350;
Best Local Similarity 38.2%; Pred. No. 4.9e-39;
Matches 121; Conservative 56; Mismatches 127; Indels 13; Gaps 6;

QY 11 NYTEEMSGDYDSMKEPCFREMANFNKIPLTIYSIIFTLGIYNGIYILVMGYOKRLR 70
DB 16 NFT---GNPDADEYDSCML-ETETLNKRYVIVIAVALVFLSLGNSLMVLIYSRGR 71
QY 71 SMTDKRYRLHSVADLFTLPEFNAVDAVAMVYGNFCKAVHYIYTVNLSSVLIILAFI 130
DB 72 SVDRLAIVHATRLITQKRYLV-KFVCLGCGLSMNLSPFLFRQAHHPNNSPVCEY 190
QY 131 SLDRLAIVHATNSQRPRLAEKVYVGVNIPALLTIIPDFIFANVSEADRY-ICDRF 189
DB 132 SVDRILAIVHATRLITQKRYLV-KFVCLGCGLSMNLSPFLFRQAHHPNNSPVCEY 190
QY 190 YPNDL--WVVFQOHIMVGLIPGIYILSCYIIISKLSHSGHOKRKALKTTVILILA 247
DB 191 LGNDTAKRMVYLRILPHTFGFIVPLFVLMFCYGFLLRFLFAHMGOKHRAMRYIAVLI 250
QY 248 EFACWLPYIGISIDSEFILLEIKOGCEFEFNTVHKMISTETALAFPHCLNPIILYAFIGA 307
DB 251 FLLCWLPPYNLVLLADTLMRTQVIOETCERRNHIGALDATEILGFLHSCNLPILYAFIQG 310
QY 308 KF-----KTSQHAULTS 319
DB 311 NFRHGFLKIILAMHGLYS 327

RESULT 15
US-08-076-093A-2
Sequence 2, Application US/08076093A
Patent No. 5543503
GENERAL INFORMATION:
APPLICANT: Chuntharapal, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Lee, James
APPLICANT: Jin Kim, K
TITLE OF INVENTION: Antibodies to Human PFA4 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-076-093A-2

Query Match 30.5%; Score 557.5; DB 1; Length 350;
Best Local Similarity 38.2%; Pred. No. 4,9e-39;
Matches 121; Conservative 56; Mismatches 127; Indels 13; Gaps 6;

QY 11 NTEEMSGSDYDSMKPEPCREENANANKIFLPITYSIIFLTGIVNGLVILVNGYOKLR 70
16 NPT--GMPPEDEDYSPCLM-ETETLNKYVVIAYVALVFLSLGNSLVMLVILYSRVGR 71
QY 71 SMTDKYRLHLSVADLLFVTLPPMAVDVAVANMYEGNLCYAVHYITVNLSSVLIAFI 130
72 SVTDVYLLNLADLLFALTLPIMASKVNGWTFGLCKVSLKEVNFSGILLIACI 131
QY 131 SLDRYLAIVHATNSORPRKLAEKVYVGVWIPALLITPDIFANVSEADRY-ICDRP 189
132 SVDRYLAIVHATRTLTQKRHLV-KFVCLGQWGLSMNLSPFLFRQAYHPNNSPCYEY 190
QY 190 YPNDL--WVVFQFOHIMGLIPGIVILSCYIITSKLSHGKHKRAKAKTTVILILA 247
191 LQNDYAKMWMVRLIPHTGFIIVPLFVMLCYGFTLRTLFKAHMGKHRAMRVIAFVVL 250
QY 248 PFACWLPYVIGISIDSFILLEIKQCEFEENTYHKWISITKALFPHCCINPLVAFGLA 307
251 FLLCWLPYVNLVLLADLTMTQVIGETCERRNNIGRALDATEIILGFLHSCINPLIYAFIGQ 310
QY 308 KF----KTSQHAITS 319
311 NFRHGFLKILAMHGLVS 327
Db

Search completed: September 14, 1999, 09:51:01
Job time: 46 sec

Human G-protein ch
African green monk

Run on: September 14, 1999, 09:50:15 ; Search time 14.3 Seconds

(without alignments)
583.043 Million cell updates/sec

Title: US-09-104-063-4
 Perfect score: 1830
 Sequence: 1 MEGISIIYTDNYTEMGSD.....KRGCHSSVSTESSESSFHSS 352

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36: *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1830	100.0	352	1	R68812	Human monocyte protein
2	1830	100.0	352	1	R80757	Chemokine superfamily
3	1819	99.4	352	1	R27792	New platelet factor
4	1808	98.8	356	1	W97362	G-protein coupled
5	1752	95.7	337	1	W48734	Human RX3 seven transmembrane
6	1742	95.2	337	1	R53753	Human RX3 seven transmembrane
7	1678.5	91.7	359	1	W64778	A murine CXCR4 chemokine receptor
8	597.5	32.7	367	1	R99247	Rodent chemokine receptor
9	578	31.6	367	1	W69999	Human IP-10/Mig receptor
10	576.5	31.5	368	1	W54311	Human IP-10/Mig receptor
11	574	31.4	368	1	R80953	Recombinant high affinity IL8-R type 2-GPB 1
12	568.5	31.1	1064	1	R70124	Sequence in a low affinity IL8-R type 2-GPB 1
13	568	31.0	360	1	R28273	Human IL-8 receptor
14	568	31.0	355	1	R33420	Human IL-8 receptor
15	568	31.0	360	1	R80758	Human G-protein coupled
16	567.5	31.0	415	1	W19780	Sequence in a high affinity recombinant high affinity
17	564	30.8	355	1	R28272	Putative seven transmembrane
18	564	30.8	355	1	R80950	Recombinant high affinity
19	560	30.6	378	1	R53744	Putative seven transmembrane
20	559.5	30.6	350	1	R27791	Recombinant high affinity
21	558	30.5	358	1	R80952	Recombinant high affinity
22	557.5	30.5	350	1	R68811	Interleukin-8 receptor
23	557.5	30.5	1060	1	R70123	IL8-R type 1-GPB 1
24	557.5	30.5	350	1	R80756	Interleukin 8 receptor
25	557.5	30.5	350	1	R80951	Recombinant high affinity
26	557	30.5	410	1	R53743	Putative seven transmembrane
27	557	30.4	358	1	R53745	Partial sequence of
28	557	30.4	410	1	W48723	Polypeptide sequence of
29	557	30.4	378	1	W48724	Human V31 seven transmembrane
30	550	30.1	359	1	R53747	Seven transmembrane
31	550	30.1	359	1	W48728	Murine V31 seven transmembrane
32	549.5	30.0	355	1	R53748	Seven transmembrane
33	549.5	30.0	355	1	W48722	Human V28 seven transmembrane
34	543	29.7	358	1	R28274	Sequence in a low affinity
35	540	29.5	372	1	R27793	New platelet factor
36	540	29.5	372	1	R68813	Human lymphocyte factor
37	540	29.5	372	1	R92239	Chemokine superfamily
38	538	29.4	378	1	R54079	Epstein Barr virus
39	538	29.4	378	1	W56164	G-protein coupled
40	538	28.9	374	1	W53622	Epstein Barr virus
41	528	28.9	355	1	R79165	Human monocyte chemokine
42	528	28.9	355	1	W56689	Human MCP-4 receptor
43	527	28.8	355	1	W07618	Human G-protein coupled

ALIGNMENTS

RESULT 1

R68812

ID R68812 standard: Protein: 352 AA.

AC R68812;

DT 18-JUL-1995 (first entry)

DE Human monocyte PF4AR.

KW Interleukin-8 receptor; IL-8 receptor; PF4AR;

KW platelet factor superfamily receptor; monocyte; chemotactic;

KW inflammation; inflammatory disease; arthritis; emphysema; cystic

KW fibrosis; colitis; bronchitis; meningitis; therapeutic.

OS Homo sapiens.

PN M09428931-AA.

PD 22-DEC-1994.

PF 07-JUN-1994; U06380.

PR 11-JUN-1993; U5-076093.

PA (GERTH) GENENTECH INC.

PI Chantharapal A, Hebert C, Kim KJ, Lee J;

DR WPI: 95-036114/05.

N-PSDB: Q80521.

DR Treatment of inflammatory disorders - by administering an

PT antibody capable of binding a platelet factor 4 superfamily

PT receptor polypeptide

CS Disclosure: Page 54-56; 83pp; English.

CC 2 PF4AR members were identified by probing lambda libraries from

CC human monocyte-like cell line HL-60 and human peripheral blood

CC lymphocytes using a large fragment of IL-8 receptor DNA (full

CC sequence given in Q80520). The nucleotide sequences of the 2

CC PF4ARs are given in Q80521 and Q80522, and their respective

CC amino acid sequences in R68812 and R68813.

Q0 Sequence 352 AA;

Query Match	100.0%;	Score 1330;	D2 1;	Length 352;
Best Local Similarity	100.0%;	Pred. No. 2.1e-212;		
Matches 352;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MEGISIYSDNYTEMGSGDVSKKEPCQFRENNANFNKIFLPTIYSLIFLTGIVGNLVI	60
Db	1	MEGISIYSDNYTEMGSGDVSKKEPCQFRENNANFNKIFLPTIYSLIFLTGIVGNLVI	60
QY	61	LYMGYOKKLRSMTQRYRLHLSVADLLVYITLPEFAVAQAVANMYGNGFLCAVHIYTVNL	120
Db	61	LYMGYOKKLRSMTQRYRLHLSVADLLVYITLPEFAVAQAVANMYGNGFLCAVHIYTVNL	120
QY	121	YSSVLLIAFLISLDRIYLAIVHATNSQDRPKLLAEKVYVGVVWIPALLTIPDFIFANYSEA	180
Db	121	YSSVLLIAFLISLDRIYLAIVHATNSQDRPKLLAEKVYVGVVWIPALLTIPDFIFANYSEA	180
QY	181	DDRIYICDRFYFNDLMVYVFGQPHIMVGLILPGYIYLSCYCIISKLSHSGHOKRKALKT	240
Db	181	DDRIYICDRFYFNDLMVYVFGQPHIMVGLILPGYIYLSCYCIISKLSHSGHOKRKALKT	240
QY	241	TVIIILIAFAACMLYYIYGISIDSFILILEIIKOGCEFNNTYHKMISITELAAFFHCCLNPI	300
Db	241	TVIIILIAFAACMLYYIYGISIDSFILILEIIKOGCEFNNTYHKMISITELAAFFHCCLNPI	300
QY	301	LYAFILGAKFKTSAQHALLTSVSRGSSLLKILSKGRGSHSSVSTESSSSFHSS 352	
Db	301	LYAFILGAKFKTSAQHALLTSVSRGSSLLKILSKGRGSHSSVSTESSSSFHSS 352	
RESULT	2		
R80757			
ID	R80757	standard: Protein: 352 AA.	
AC	R80757:		
DT	26-MAR-1996	(first entry)	

DE Chemokine superfamily receptor.
 KW Interleukin: IL-8; inflammation; psoriasis; dermatitis;
 KW rheumatoid arthritis; inflammatory bowel disease;
 KW chronic lung inflammation; treatment; antibody;
 KW affinity purification; detection.
 OS Homo sapiens.
 PN US5440021-A.
 PD 08-AUG-1995.
 PE 29-MAR-1991; 677211.
 PR 29-MAR-1991; US-677211.
 PA (CHUN)/ CHUNTHARAPAI A.
 PA (HEBE)/ HEBERT C.
 PA (KIMK)/ KIM K J.
 PA (LEEJ)/ LEE J.
 PI Chuntharapai A, Hebert C, Kim KJ, Lee J;
 PI WPI: 95-283151/37.
 DR N-PSDB: Q29007.
 DR New antibodies against interleukin 8 type B receptor - used to treat
 PT or prevent inflammation, also for detecting receptor expression and
 PT purification.
 PS Example 2: Columns 45-48: 62pp: English.
 CC Antibodies directed against the interleukin-8 receptor B can be used
 CC to treat or prevent inflammation e.g. psoriasis, dermatitis,
 CC rheumatoid arthritis and particularly inflammatory bowel disease and
 CC chronic lung inflammation. When immobilised, these antibodies may
 CC be used to detect interleukin-8 receptor B expression in cells and
 CC tissues and for affinity purification of interleukin-8 receptor B
 CC from cells. This sequence is an additional chemokine superfamily
 CC receptor which was identified by probing lambda libraries of genomic
 CC DNA from a human monocytic-like cell line (U-60) and human peripheral
 CC blood lymphocytes using a large fragment of the interleukin-8 type
 CC A receptor DNA (See Q99006).
 SQ Sequence 352 AA:

Query Match 100.0%; Score 1830; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.1e-212;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITSDNTEEMSGDYSKMEPCFREANFNKIFLPTIYSIFLTGIVNGLVI 60
 DB 1 MEGISITSDNTEEMSGDYSKMEPCFREANFNKIFLPTIYSIFLTGIVNGLVI 60
 QY 61 LVNGYOKKLRSMYDKYRLHLSTADLLFVITLPPWADVANNYFGNLCRAVHIYTVNL 120
 DB 61 LVNGYOKKLRSMYDKYRLHLSTADLLFVITLPPWADVANNYFGNLCRAVHIYTVNL 120
 QY 121 YSSVLLAFISLDRIYAIYHATNSQRPRLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
 DB 121 YSSVLLAFISLDRIYAIYHATNSQRPRLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
 QY 181 DDRYICDRFPNDLMVWVFOFQHMVGLILPGVILSCYCIILSKSHSGHOKRAKLT 240
 DB 181 DDRYICDRFPNDLMVWVFOFQHMVGLILPGVILSCYCIILSKSHSGHOKRAKLT 240
 QY 241 TVILLIAFFACWLPYYIGISIDSFILLEIKQCEFEENTVHKWISTEALAFHCCLNPI 300
 DB 241 TVILLIAFFACWLPYYIGISIDSFILLEIKQCEFEENTVHKWISTEALAFHCCLNPI 300
 QY 301 LYAFLGAKFRTSAQHALTSVRGSSSLKILSKGRGSHSVTESSSFHSS 352
 DB 301 LYAFLGAKFRTSAQHALTSVRGSSSLKILSKGRGSHSVTESSSFHSS 352

RESULT 3
 R27792
 ID R27792 standard; Protein: 352 AA.
 AC R27792;
 DT 12-MAR-1993 (first entry)
 DE New platelet factor 4 receptor superfamily member PF4AR1.
 KW IL-8R; G-protein coupled receptor family; rhodopsin superfamily;
 KW pro-inflammatory cytokine; 8rr.20.15.

OS Homo sapiens.
 PN W09217497-A.
 PD 13-OCT-1992.
 PE 23-MAR-1992; U02317.
 PR 29-MAR-1991; US-677211.
 PR 19-DEC-1991; US-810782.
 PA (GETH) GENENTECH INC.
 PA Holmes WE, Lee J, Wood WI;
 PI WPI: 92-366191/44.
 DR N-PSDB: Q29506.
 DR Isolated human platelet factor 4 super-family receptor
 PT polypeptide and corresp. antibodies and DNA - useful as
 PT diagnostic and screening agents, and for treating inflammation or
 PT PF4AR-mediated disorders
 PS Claim 7: Fig 4: 78pp: English.
 CC The IL-8 receptor cDNA sequence was isolated (see Q29505) and a
 CC 874bp sub-fragment of the coding sequence was used as a probe to
 CC screen human cell line HL60 and human peripheral blood lymphocyte
 CC cDNA libraries. Two new gene sequences were found that are clearly
 CC related to the IL-8 receptor. One of these was contained in
 CC combined clone 8rr.20.15 and is predicted to encode an amino acid
 CC sequence which is 34% identical with both the high and low affinity
 CC IL-8 receptors. See also Q37107.
 SQ Sequence 352 AA:

Query Match 99.4%; Score 1819; DB 1; Length 352;
 Best Local Similarity 99.7%; Pred. No. 4.5e-211;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEGISITSDNTEEMSGDYSKMEPCFREANFNKIFLPTIYSIFLTGIVNGLVI 60
 DB 1 MEGISITSDNTEEMSGDYSKMEPCFREANFNKIFLPTIYSIFLTGIVNGLVI 60
 QY 61 LVNGYOKKLRSMYDKYRLHLSTADLLFVITLPPWADVANNYFGNLCRAVHIYTVNL 120
 DB 61 LVNGYOKKLRSMYDKYRLHLSTADLLFVITLPPWADVANNYFGNLCRAVHIYTVNL 120
 QY 121 YSSVLLAFISLDRIYAIYHATNSQRPRLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
 DB 121 YSSVLLAFISLDRIYAIYHATNSQRPRLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
 QY 181 DDRYICDRFPNDLMVWVFOFQHMVGLILPGVILSCYCIILSKSHSGHOKRAKLT 240
 DB 181 DDRYICDRFPNDLMVWVFOFQHMVGLILPGVILSCYCIILSKSHSGHOKRAKLT 240
 QY 241 TVILLIAFFACWLPYYIGISIDSFILLEIKQCEFEENTVHKWISTEALAFHCCLNPI 300
 DB 241 TVILLIAFFACWLPYYIGISIDSFILLEIKQCEFEENTVHKWISTEALAFHCCLNPI 300
 QY 301 LYAFLGAKFRTSAQHALTSVRGSSSLKILSKGRGSHSVTESSSFHSS 352
 DB 301 LYAFLGAKFRTSAQHALTSVRGSSSLKILSKGRGSHSVTESSSFHSS 352

RESULT 4
 W97362
 ID W97362 standard; Protein: 356 AA.
 AC W97362;
 DT 12-MAY-1999 (first entry)
 DE G-protein coupled receptor polypeptide designated CXCR4B.
 KW G-protein coupled receptor; CXCR4B; human; splice variant;
 KW chemokine receptor; CXCR4; vaccine; gene therapy; HIV-1;
 KW cancer; pain; diabetes; obesity; anorexia; bulimia; asthma;
 KW Parkinson's disease; acute heart failure; hypotension; hypertension;
 KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
 KW stroke; ulcer; allergy; benign prostatic hypertrophy; migraine;
 KW vomiting; psychotic disorder; neurological disorder; anxiety;
 KW schizophrenia; manic depression; delirium; dementia; mental retardation;
 KW dyskinesias; Huntington's disease; Gilles de la Tourette syndrome.
 OS Homo sapiens.
 PN EP-897980-A2.
 PD 24-FEB-1999.

[illegible]

diagnostically and therapeutically to treat conditions associated with abnormal physiology or development e.g. inflammatory conditions.

Claim 4; Pages 89-92; 105pp; English.

This represents a rodent chemokine receptor HST01.1 amino acid sequence. The invention provides novel primate and rodent chemokines and chemokine receptors. The chemokines, receptors and binding compounds (optionally antibodies/fragments specifically binding the chemokines) are useful therapeutically to treat conditions associated with abnormal physiology or development e.g. inflammatory conditions such as asthma. Chemokines are important in immune and inflammatory responses in that they induce leukocyte migration and adhesion. They are also chemottractants for several cells involved in inflammation and can induce other biological responses e.g. modulation of second messenger levels (e.g. Ca^{++}), lipid cellular morphology modification responses etc. The chemokine receptors of turnover, possible antiviral responses etc. The chemokine receptors of the invention possess structural properties of G-protein coupled receptors (GPCR), although their ligands have not yet been identified.

The chemokine and chemokine receptor polypeptides are useful to produce ligand:receptor complexes in vivo or in assay techniques. Assays may also involve chemical antagonists which block complex production or utilize competitive binding. Binding compounds identified (agonists or antagonists) can be used to modulate the physiological responses in cells (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal proliferation, regeneration, generation and atrophy. The polypeptides are also used to produce antibodies useful diagnostically, for drug screening or for polypeptide purification. The polynucleotides are useful to produce probes for detecting the polypeptides, and to isolate the polypeptides or related sequences, especially from other species. They also allow transformation of cells for polypeptide production.

Sequence 367 AA;

Query Match	31.68;	Score 578;	DB 1;	Length 357;
Best Local Similarity	35.38;	Pred. No. 2.6e-61;		
Matches 120;	Conservative 71;	Mismatches 133;	Indels 16;	Gaps 6;
QY 15	EMGSGDYD-SMKEPCEFRNANFNKIFLPTYSIIIFLTGIVNGVLVYNGYKRLRSMT	73		
Db 28	DVGENSDSDSPPCPPQDSFLNDFTLFLPALYSILFLTGLIGNCAVAAYLSQRTALSRT	87		
QY 74	DKYRLHLVSADLLFLVITLPEFMAVDAVANWYGNFLCAVHYTVYVNYSSVLLIAFSLD	133		
Db 88	DFFLHLAAVDVILVLTPLPMVADAAVOMVGPGLCKVAGALFININYPAGAFLLACISFD	147		
QY 134	RYATVYHAINSOR--PRKLLAEKVVYGVYPMALITLTPDIF--ANYSEADRYICDRF	189		
Db 148	RYSTVYHATQYIRKDDPRVYA--LNCIYVWGCLLFLALPDLYLSANYDQRLNATHCOYN	205		
QY 190	YPNDLWVYVFOFOHIVGILPEGVILSCYIIISKLSHGOKRKLKTTVILLIAFE	249		
Db 206	FP-QVGTALRYQLVAGFLLPLVWACYAHILLVLLVSRCQRFRRMRRLVVVYAAFA	264		
QY 250	ACWLPRYTGISIDSFILLEIKOGCEFTVYKMTISFEALAFEFCCNPLIYAFLGAKF	309		
Db 265	VCWMPYHLVVLVILMDVGLNACNGCRKSHVDYANSYISGMGYMCCNPLIYAFVGVKF	324		
QY 310	KTSAQHALTSVSRGSSILKILSKGRGSHSVYTESSESF	349		
Db 325	REKMMMLFTRLGRSD-----QRGPQRQPSSSRRESSW	356		
RESULT 10				
W54371				
ID W54371 standard; Protein: 368 AA.				
AC W54371:				
DT 14-AUG-1998 (first entry)				
DE Human IP-10/Mig receptor CXCR3 protein.				
KW chemokine receptor; cellular signal; treatment; T cell; antitumour;				
OS antiviral; inflammatory disease.				
KS Homo sapiens.				
FT Key Location/Qualifiers				
FT Modified_site 22				
FT /note= "N-linked glycosylation site"				

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OM nucleic - nucleic search, using sw model

Run on: September 14, 1999, 09:53:45 ; Search time 47.19 Seconds
(without alignments)
9209.232 Million cell updates/sec

Title: US-09-104-063-3
Perfect score: 1737
Sequence: 1 GAATTCAGTGTCTGCTGGCGG.....CCGCCAGACACTGGAAATTC 1737

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1737	100.0	1737	1	Human monocytic PF4
2	1737	100.0	1737	1	Chemokine superfamily
3	1730.6	99.6	1737	1	New platelet factor
4	1569.2	90.3	1944	1	CDNA encoding G-pro
5	1118.2	64.4	1317	1	Human RM3 seven tr
6	1118.6	64.3	1317	1	Seven transmembran
7	974.4	56.1	1877	1	Nucleic acid encod
8	249	14.3	611	1	CDNA encoding a pa
9	218	12.6	218	1	Human gene signatu
10	206.8	11.9	1200	1	Sequence encoding
11	206.8	11.9	1200	1	Recombinant high a
12	202.2	11.6	1373	1	Recombinant high a
13	196.8	11.3	1933	1	Interleukin-8 rece
14	196.8	11.3	1933	1	Interleukin-8 rece
15	196.8	11.3	1883	1	Interleukin-8 rece
16	196.8	11.3	1176	1	Recombinant high a
17	196.6	11.3	2160	1	Putative seven tra
18	196.6	11.3	1900	1	Partial coding seq
19	196.6	11.3	2058	1	Putative seven tra
20	196.6	11.3	2058	1	Human V31 seven tr
21	196.6	11.3	1900	1	Human V31 seven tr
22	196.6	11.3	2160	1	Human V31 seven tr
23	193.4	11.1	1670	1	Human IP-10/Mig re
24	191.8	11.0	1876	1	Human G-protein ch
25	190.2	10.9	2154	1	Epstein Barr virus
26	190.2	10.9	2154	1	CDNA for Epstein B
27	190.2	10.9	2154	1	Sequence encoding
28	188.6	10.9	1373	1	Recombinant high a
29	184	10.6	1106	1	Sequence encoding
30	182.4	10.5	1106	1	Human IL-8 recepto
31	182.4	10.5	1310	1	Interleukin 8 (IL-
32	182.4	10.4	1299	1	Seven transmembran
33	180.8	10.3	2751	1	Murine V31 seven t
34	178.4	10.3	2751	1	Seven transmembran
35	178.4	10.2	2254	1	Seven transmembran
36	178	10.2	2254	1	Human V28 seven tr
37	178	10.2	2254	1	Human V28 seven tr
38	178	10.2	2254	1	New platelet facto
39	174.8	10.1	1679	1	Human lymphocyte P
40	174.8	10.1	1679	1	Chemokine superfam
41	174.8	10.1	1679	1	Rodent chemokine r
42	174.8	10.1	1679	1	
43	162.2	9.3	1620	1	

ALIGNMENTS

44 160.8 9.3 1586 1 T44099 Human G-protein re
45 160.8 9.3 1068 1 V28385 Human MCP-4 recept

RESULT 1	080521	080521 standard; CDNA; 1737 BP.
ID	080521;	
AC	18-JUL-1995 (first entry)	
DE	Human monocytic PF4R CDNA	
KW	Interleukin-8 receptor; IL-8 receptor; PF4R;	
KW	platelet factor superfamily receptor; monocytic; chemotactic;	
KW	inflammation; inflammatory disease; arthritis; emphysema; cystic;	
KW	fibrosis; colitis; bronchitis; meningitis; therapeutic; ss.	
OS	Homo sapiens.	
FH	Key	location/Qualifiers
FT	cds	91..1149
FT		/*tag= a
FT	W09428931.A.	
PD	22-DEC-1994.	
PR	07-JUN-1994; U06380.	
PR	11-JUN-1993; US-076093.	
PA	(GETH) GENENTECH INC.	
PI	Chuntharapal A, Hebert C, Kim KJ, Lee J.	
DR	WPI: 95-036114/05.	
DR	P-PSDB; R68812.	
PT	Treatment of inflammatory disorders - by administering an	
PT	antibody capable of binding a platelet factor 4 superfamily	
PT	receptor polypeptide	
PS	disclosure; Page 54-56; 83pp; English.	
CC	2 PF4R members were identified by probing lambda libraries from	
CC	human monocytic-like cell line HL-60 and human peripheral blood	
CC	lymphocytes using a large fragment of IL-8 receptor DNA (full	
CC	sequence given in 080520). The nucleotide sequences of the 2	
CC	PF4Rs are given in 080521 and 080522, and their respective	
CC	amino acid sequences in R68812 and R68813.	
S0	Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T;	
Query Match 100.0%; Score 1737; DB 1; Length 1737;		
Best Local Similarity 100.0%; Pred. No. 0;		
Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	GAATTCAGTGTCTGCTGGCGGCGCAAGTAGACGCCAGGCGCTGAGTCTCCAGTA 60
DB	1	GAATTCAGTGTCTGCTGGCGGCGGCGCAAGTAGACGCCAGGCGCTGAGTCTCCAGTA 60
QY	61	GCCACCGCATCTGGAGAACCGCGGTTACATGAGGGGATCAATATACACTTCAGAT 120
DB	61	GCCACCGCATCTGGAGAACCGCGGTTACATGAGGGGATCAATATACACTTCAGAT 120
QY	121	AACATACACCGAAGATGGGCTCAGGGGATGATCTCATGAGGAACCTGTTCCGT 180
DB	121	AACATACACCGAAGATGGGCTCAGGGGATGATCTCATGAGGAACCTGTTCCGT 180
QY	121	AACATACACCGAAGATGGGCTCAGGGGATGATCTCATGAGGAACCTGTTCCGT 180
DB	121	AACATACACCGAAGATGGGCTCAGGGGATGATCTCATGAGGAACCTGTTCCGT 180
QY	181	GAGGAAATGCTAATTTCAATAAATCTCTGCCACCATCTACTCCATCATCTTTCTTA 240
DB	181	GAGGAAATGCTAATTTCAATAAATCTCTGCCACCATCTACTCCATCATCTTTCTTA 240
QY	241	ACTGGCATTTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB	241	ACTGGCATTTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY	301	AGCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 360
DB	301	AGCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 360
QY	361	CTTCCCTTTCTGGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB	361	CTTCCCTTTCTGGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

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OY 421 GCAGTCATGTCATCTACACAGTCACCTCTACAGAGTGTCTCTACCTGCGGCTTCATC 480
    |||||||
Db 421 GCAGTCATGTCATCTACACAGTCACCTCTACAGAGTGTCTCTACCTGCGGCTTCATC 480
OY 481 AGTCTGAGCGCTACCTGGCCATGTCACAGCCACCAAGTCAGAGGCCAAGAGCTG 540
    |||||||
Db 481 AGTCTGAGCGCTACCTGGCCATGTCACAGCCACCAAGTCAGAGGCCAAGAGCTG 540
OY 541 TTGGCTGAAAAGGTGTCTATGTTGGGCTGTGGATCCCTGCGCTGATATTTCC 600
    |||||||
Db 541 TTGGCTGAAAAGGTGTCTATGTTGGGCTGTGGATCCCTGCGCTGATATTTCC 600
OY 601 GACTTATCTTTGCCAAGCTGACAGGAGCATGATATATCTGTGACCGCTTCTAC 660
    |||||||
Db 601 GACTTATCTTTGCCAAGCTGACAGGAGCATGATATATCTGTGACCGCTTCTAC 660
OY 661 CCCAATGACTTGTGGGTGTGTTGTTCCAGTTTCAGCACATCATGTTGGCTTATCTG 720
    |||||||
Db 661 CCCAATGACTTGTGGGTGTGTTGTTCCAGTTTCAGCACATCATGTTGGCTTATCTG 720
OY 721 CCTGTATGTCTATCTCTGTCTCTATGATATATCTCTCCAAAGCTGTACACTCCAG 780
    |||||||
Db 721 CCTGTATGTCTATCTCTGTCTCTATGATATATCTCTCCAAAGCTGTACACTCCAG 780
OY 781 GGGCAGCAGAGAGCGCAAGGCCCTCAAGACCAAGTCATCTCTACCTGCTTCTGCGC 840
    |||||||
Db 781 GGGCAGCAGAGAGCGCAAGGCCCTCAAGACCAAGTCATCTCTACCTGCTTCTGCGC 840
OY 841 TGTGTGCTGCTTACTACATTTGGGATCAGCATGACTCTCTTCACTCTGTAATCATC 900
    |||||||
Db 841 TGTGTGCTGCTTACTACATTTGGGATCAGCATGACTCTCTTCACTCTGTAATCATC 900
OY 901 AAGCAAGGGGTGAGTTTGGAGAACCTGTGCACAAAGTGGATTCACACGAGGCCCTA 960
    |||||||
Db 901 AAGCAAGGGGTGAGTTTGGAGAACCTGTGCACAAAGTGGATTCACACGAGGCCCTA 960
OY 961 GCTTTCTTCACATGTTGTCTGAAGCCCATCTCTATGCTTCTGAGGCCAATTTAA 1020
    |||||||
Db 961 GCTTTCTTCACATGTTGTCTGAAGCCCATCTCTATGCTTCTGAGGCCAATTTAA 1020
OY 1021 ACCTGTGCCAGCAGCAGCTACCTCTGTGAGCAGAGGGTCCAGCCTCAAGCTCTCC 1080
    |||||||
Db 1021 ACCTGTGCCAGCAGCAGCTACCTCTGTGAGCAGAGGGTCCAGCCTCAAGCTCTCC 1080
OY 1081 AAGGAAAGGAGGTGACATCTGTTCCAGTGAAGTCTGAAGTCTTCAAGTTTTCAC 1140
    |||||||
Db 1081 AAGGAAAGGAGGTGACATCTGTTCCAGTGAAGTCTGAAGTCTTCAAGTTTTCAC 1140
OY 1141 TCCAGCTAACACAGATGTAAGACCTTTTATAGATAAATTAATCTTTTAAAGT 1200
    |||||||
Db 1141 TCCAGCTAACACAGATGTAAGACCTTTTATAGATAAATTAATCTTTTAAAGT 1200
OY 1201 ACACATTTTTCAGATATAAAGACTGCACAAATATGTACAGTTTATGCTGTTGGAT 1260
    |||||||
Db 1201 ACACATTTTTCAGATATAAAGACTGCACAAATATGTACAGTTTATGCTGTTGGAT 1260
OY 1261 TTTTGTCTGTGTTCTTTGTTTGTGTAAGTTTAAATTAATTAATTAATTTT 1320
    |||||||
Db 1261 TTTTGTCTGTGTTCTTTGTTTGTGTAAGTTTAAATTAATTAATTAATTTT 1320
OY 1321 TTTGTTTCATTTGATGTGTGTAGCAGAGACCTGTGGCAAGTCTTGTGCTGTAT 1380
    |||||||
Db 1321 TTTGTTTCATTTGATGTGTGTAGCAGAGACCTGTGGCAAGTCTTGTGCTGTAT 1380
OY 1381 GTCTCGTGTAGAGCTGTAGAAAAAGGAACTGAACATTCAGAGCGGTAGTGAATCAG 1440
    |||||||
Db 1381 GTCTCGTGTAGAGCTGTAGAAAAAGGAACTGAACATTCAGAGCGGTAGTGAATCAG 1440
OY 1441 TAAAGCTAGAAATGATCCCAAGCTGTTTATGATAGATAATCTCTCATTCCTGCTGAG 1500
    |||||||
Db 1441 TAAAGCTAGAAATGATCCCAAGCTGTTTATGATAGATAATCTCTCATTCCTGCTGAG 1500

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OY 1501 GTTTTCCGTGTTCTTAAAGAGTATTTGCTGTAGAAAGTGCACCTTAAACAAAGCCC 1560
    |||||||
Db 1501 GTTTTCCGTGTTCTTAAAGAGTATTTGCTGTAGAAAGTGCACCTTAAACAAAGCCC 1560
OY 1561 AAAGTGTATAGAAATGCTGTTTTCAGTTTTCAGAGAGTGGGTTGATTTCAGCACCTAC 1620
    |||||||
Db 1561 AAAGTGTATAGAAATGCTGTTTTCAGTTTTCAGAGAGTGGGTTGATTTCAGCACCTAC 1620
OY 1621 AGTGTACAGTCTTGTATAGTTGTATTAATAAGTACATGTTAACTTAAAAA 1680
    |||||||
Db 1621 AGTGTACAGTCTTGTATAGTTGTATTAATAAGTACATGTTAACTTAAAAA 1680
OY 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCAGCAGCACATGGAATTC 1737
    |||||||
Db 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCAGCAGCACATGGAATTC 1737

RESULT 2
ID O99007 standard; cDNA; 1737 BP.
AC O99007:
DT 26-MAR-1996 (first entry)
DE Chemokine superfamily receptor coding sequence.
KW Interleukin; IL-8; inflammation; psoriasis; dermatitis;
KW rheumatoid arthritis; inflammatory bowel disease;
KW chronic lung inflammation; treatment; antibody;
KW affinity purification; detection; ss.
OS Homo sapiens.
PN US3440021.A.
PD 08-AUG-1995.
PF 29-MAR-1991; 677211.
PR 29-MAR-1991; US-677211.
PR 25-FEB-1994; US-202056.
PA (CHUN/) CHUNTHARAPAI A.
PA (HEBE/) HERBERT C.
PA (KIM/) KIM K J.
PA (LEEJ/) LEE J.
PI Chuntharapai A., Herbert C., Kim KJ, Lee J;
PI MPI: 95-283151/37.
DR P-PSDB: R80757.
PT New antibodies against interleukin 8 type B receptor - used to treat
PT or prevent inflammation, also for detecting receptor expression and
PT purification.
PS Example 2; Columns 47-50; 62pp; English.
CC Antibodies directed against the interleukin-8 receptor B can be used
CC to treat or prevent inflammation e.g. psoriasis, dermatitis,
CC rheumatoid arthritis and particularly inflammatory bowel disease and
CC chronic lung inflammation. When immobilised, these antibodies may
CC be used to detect interleukin-8 receptor B expression in cells and
CC tissues and for affinity purification of interleukin-8 receptor B
CC from cells. This sequence is an additional chemokine superfamily
CC receptor which was identified by probing lambda libraries of genomic
CC DNA from a human monocyte-like cell line (L-60) and human peripheral
CC blood lymphocytes using a large fragment of the interleukin-8 type
CC A receptor DNA (see O99006).
SQ Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T;

Query Match 100.0%; Score 1737; DB 1; Length 1737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAATTCACATGTCGTCGGCGCGCGCAAGTGAACGCGAGGCTGAGTCTCCAGTA 60
    |||||||
Db 1 GAATTCACATGTCGTCGGCGCGCGCAAGTGAACGCGAGGCTGAGTCTCCAGTA 60
OY 61 GCCACGCACTCTGAGAAACACAGCGTTACATGAGAGGGATCATATATACACTTCAGAT 120
    |||||||
Db 61 GCCACGCACTCTGAGAAACACAGCGTTACATGAGAGGGATCATATATACACTTCAGAT 120
OY 121 AACTACACCGAGAAATGGGCTCAGGGGACTATGACTCCATGAGAAACCTGTTCCGT 180
    |||||||
Db 121 AACTACACCGAGAAATGGGCTCAGGGGACTATGACTCCATGAGAAACCTGTTCCGT 180

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QY 181 GAAGAAATGCTAATTCATAAATCTCTCTGCGCAACATCTACTGCATCATCTTCTTA 240
 DB 181 GAAGAAATGCTAATTCATAAATCTCTCTGCGCAACATCTACTGCATCATCTTCTTA 240
 QY 241 ACTGGCATTTGGGCAATGATTTGGTCATCCTGGTCATGGTTACGAAGAAGAACTGAGA 300
 DB 241 ACTGGCATTTGGGCAATGATTTGGTCATCCTGGTCATGGTTACGAAGAAGAACTGAGA 300
 QY 301 AGCATGACGACAACTACAGAGCTGACCTGTCACTGGCCGACCTCTCTTTGTATCAGC 360
 DB 301 AGCATGACGACAACTACAGAGCTGACCTGTCACTGGCCGACCTCTCTTTGTATCAGC 360
 QY 361 CTTCCTCTTGGGCAATGATTTGGTCATCCTGGTCATGGTTACGAAGAAGAACTGAGA 420
 DB 361 CTTCCTCTTGGGCAATGATTTGGTCATCCTGGTCATGGTTACGAAGAAGAACTGAGA 420
 QY 421 GCATGTCATGTCATCTACAGAGCTGACCTGTCACTGGCCGACCTCTCTTTGTATCAGC 480
 DB 421 GCATGTCATGTCATCTACAGAGCTGACCTGTCACTGGCCGACCTCTCTTTGTATCAGC 480
 QY 481 AGTGTGACCGCTACCTGGCCATGTCACAGCCCAACAGTCAAGTCACTGGCCGACCTCT 540
 DB 481 AGTGTGACCGCTACCTGGCCATGTCACAGCCCAACAGTCAAGTCACTGGCCGACCTCT 540
 QY 541 TTGGCTGAAAGAGTGTCTATGTTGGCGTCTGATCCCTGCGCTCTGATCTATCTCC 600
 DB 541 TTGGCTGAAAGAGTGTCTATGTTGGCGTCTGATCCCTGCGCTCTGATCTATCTCC 600
 QY 601 GACTTCATCTTTGGCAACGTCAGTGGAGCAGATGACAGATATATCTGTGACCGGTTCTAC 660
 DB 601 GACTTCATCTTTGGCAACGTCAGTGGAGCAGATGACAGATATATCTGTGACCGGTTCTAC 660
 QY 661 CCCATGACTCTGGGAGTGTCTGATTTGGCATTTGACACATCATGTTGGCCTTATCTG 720
 DB 661 CCCATGACTCTGGGAGTGTCTGATTTGGCATTTGACACATCATGTTGGCCTTATCTG 720
 QY 721 CCTGATTTGTCATCTCTGCTGCTGATTTGATTCATCTCAAGTGTGACACTGCAAG 780
 DB 721 CCTGATTTGTCATCTCTGCTGCTGATTTGATTCATCTCAAGTGTGACACTGCAAG 780
 QY 781 GGGCACCAGAGGCGACAGGCCCTCAGACCAAGTCACTCTGCTGCTTTCTTGCC 840
 DB 781 GGGCACCAGAGGCGACAGGCCCTCAGACCAAGTCACTCTGCTGCTTTCTTGCC 840
 QY 841 TGTGGTGTCTACTACTGATTTGGATGAGATGACATCTCTTCACTCTCTGGAATATCTC 900
 DB 841 TGTGGTGTCTACTACTGATTTGGATGAGATGACATCTCTTCACTCTCTGGAATATCTC 900
 QY 901 AAGCAAGGAGTGTGATTTGAGACACTGTGACAGTGGATTTCCATCAGGAGGCCCTA 960
 DB 901 AAGCAAGGAGTGTGATTTGAGACACTGTGACAGTGGATTTCCATCAGGAGGCCCTA 960
 QY 961 GCTTTCTTCACGTGTGTCTGAAACCCCATCTCTATGCTTTCTTGGAGCCAAATTTAAA 1020
 DB 961 GCTTTCTTCACGTGTGTCTGAAACCCCATCTCTATGCTTTCTTGGAGCCAAATTTAAA 1020
 QY 1021 ACCTTGCCAGCAGCAGCTCACCTGTGAGAGAGGAGGTCGAGCCCAAGATCTCTGTC 1080
 DB 1021 ACCTTGCCAGCAGCAGCTCACCTGTGAGAGAGGAGGTCGAGCCCAAGATCTCTGTC 1080
 QY 1081 AAGGAAAGGAGGAGTGTGATCTATCTGTTCCAGTGTGAGTGTGAGTGTGAGTGTGAG 1140
 DB 1081 AAGGAAAGGAGGAGTGTGATCTATCTGTTCCAGTGTGAGTGTGAGTGTGAGTGTGAG 1140
 QY 1141 TCCAGCTAACAGAGTGTGATCTATCTGTTCCAGTGTGAGTGTGAGTGTGAGTGTGAG 1200
 DB 1141 TCCAGCTAACAGAGTGTGATCTATCTGTTCCAGTGTGAGTGTGAGTGTGAGTGTGAG 1200
 QY 1201 ACACATTTTTCAGATATATAAGACTGACCAATATGTGACAGTGTGATTTTCTGTTGAT 1260
 DB 1201 ACACATTTTTCAGATATATAAGACTGACCAATATGTGACAGTGTGATTTTCTGTTGAT 1260

QY 1261 TTTTGTCTGTGTTCTTCTTGTAGTTTGTGAGTTTAACTTATTTATATAATTTT 1320
 DB 1261 TTTTGTCTGTGTTCTTCTTGTAGTTTGTGAGTTTAACTTATTTATATAATTTT 1320
 QY 1321 TTTTGTCTTATTTAGTGTGTGTAGGACAGCTGTGGCCAGTCTTGTGTTGCTGAT 1380
 DB 1321 TTTTGTCTTATTTAGTGTGTGTGTAGGACAGCTGTGGCCAGTCTTGTGTTGCTGAT 1380
 QY 1381 GTCTGTGTGTAGGACAGT 1440
 DB 1381 GTCTGTGTGTAGGACAGT 1440
 QY 1441 TAAAGCTAGAAATGATCCCAAGCTGTTATGATGATGATGATGATGATGATGATGATG 1500
 DB 1441 TAAAGCTAGAAATGATCCCAAGCTGTTATGATGATGATGATGATGATGATGATGATG 1500
 QY 1501 GTTTTCTCTTGT 1560
 DB 1501 GTTTTCTCTTGT 1560
 QY 1561 AAGTGTATAGAAATGCTGT 1620
 DB 1561 AAGTGTATAGAAATGCTGT 1620
 QY 1621 AGTGTACAGTCTGT 1680
 DB 1621 AGTGTACAGTCTGT 1680
 QY 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACGACACTGGAATTC 1737
 DB 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACGACACTGGAATTC 1737

RESULT 3
 Q29506
 ID Q29506 standard; DNA: 1737 BP.
 AC Q29506;
 DT 12-MAR-1993 (first entry)
 DE New platelet factor 4 receptor superfamily member PF4AR1.
 KW IL-8R; G-protein coupled receptor family; rhodopsin superfamily;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 91..1149
 FT cds
 PN W09217497-A.
 PD 15-OCT-1992.
 PF 23-MAR-1992; U02317.
 PR 29-MAR-1991; US-677211.
 PR 19-DEC-1991; US-810782.
 PA (GETH) GENENTECH INC.
 PI Holmes WE, Lee J, Wood WI;
 DR WPI; 92-366191/74.
 DR P-PSDB; R27792.
 PT Isolated human platelet factor 4 superfamily receptor
 PT polypeptide and corresp. antibodies and DNA - useful as
 PT diagnostic and screening agents, and for treating inflammation or
 PT PF4AR-mediated disorders
 CC Claim 7; Fig 4; 78pp; English.
 CC The IL-8 receptor cDNA sequence was isolated (see Q29505) and a
 CC 874bp sub-fragment of the coding sequence was used as a probe to
 CC screen human cell line HU60 and human peripheral blood lymphocyte
 CC cDNA libraries. Two new gene sequences were found that are clearly
 CC related to the IL-8 receptor. One of these was contained in
 CC combined clone 8tr.20.15 and is predicted to encode an amino acid
 CC sequence which is 34% identical with both the high and low affinity
 CC IL-8 receptors. See also Q37107.
 SO Sequence 1737 BP; 457 A; 412 C; 370 G; 498 T;

Query Match 99.6%; Score 1730.6; DB 1; Length 1737;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1733: Conservative 0; Mismatches 4; Indels 0; Gaps 0;				
QY	1	GAATTCATGTGCTGGCGCGCGGCAAGTACGCGGAGGCGCTGAGTCTCCAGTA	60	
DB	1	GAATTCATGTGCTGGCGCGCGGCAAGTACGCGGAGGCGCTGAGTCTCCAGTA	60	
QY	61	GCCACCGCATCTGGAGAACGAGCGGTACCATGAGAGGATCATGATATACACTTCAGAT	120	
DB	61	GCCACCGCATCTGGAGAACGAGCGGTACCATGAGAGGATCATGATATACACTTCAGAT	120	
QY	121	AACATACCCGAGAGAAATGGGCTCAGGGAGTATGACTCCATGAGAGAACCTGTTCGT	180	
DB	121	AACATACCCGAGAGAAATGGGCTCAGGGAGTATGACTCCATGAGAGAACCTGTTCGT	180	
QY	181	GAGAAATATGCTATTTCAATAAATCTCCGCGACATGACATCCATCTCTTA	240	
DB	181	GAGAAATATGCTATTTCAATAAATCTCCGCGACATGACATCCATCTCTTA	240	
QY	241	ACTGCGATTGTGGCAATGATGTCATCTGGTATGGGTTACGAGAAACTGAGA	300	
DB	241	ACTGCGATTGTGGCAATGATGTCATCTGGTATGGGTTACGAGAAACTGAGA	300	
QY	301	AGCATGACGAGACATGACAGGCTGACCTGTAGTGGCCGACCTCTTTGTATCAGC	360	
DB	301	AGCATGACGAGACATGACAGGCTGACCTGTAGTGGCCGACCTCTTTGTATCAGC	360	
QY	361	CTTCCCTTGTGGGCAATGATGCGGTGGCAACTGTACTTTGGAACTCCATCTGCAAG	420	
DB	361	CTTCCCTTGTGGGCAATGATGCGGTGGCAACTGTACTTTGGAACTCCATCTGCAAG	420	
QY	421	GCAGTCATGTCTATCTACACAGTCACTCTACAGCATGTCTCTACCTCGGCTTCATC	480	
DB	421	GCAGTCATGTCTATCTACACAGTCACTCTACAGCATGTCTCTACCTCGGCTTCATC	480	
QY	481	AGTCTTGACCCGCTACCTGGCATCTGCCAGCCACCAAGTACAGAGCCCAAGAGCTG	540	
DB	481	AGTCTTGACCCGCTACCTGGCATCTGCCAGCCACCAAGTACAGAGCCCAAGAGCTG	540	
QY	541	TTGGCTGAAAAGGTGGTCTATGTTGGGCTGTGGATCCGCTCTCTGCTGACTATCCG	600	
DB	541	TTGGCTGAAAAGGTGGTCTATGTTGGGCTGTGGATCCGCTCTCTGCTGACTATCCG	600	
QY	601	GACTTCATCTTTCACAGCTCACTGAGGAGATGACAGATATATCTGTGACGCTTCTAC	660	
DB	601	GACTTCATCTTTCACAGCTCACTGAGGAGATGACAGATATATCTGTGACGCTTCTAC	660	
QY	661	CCCAATGACTTGTGGGTGTGTTCCAGTTTCACACATCATGCTGCTTATCTCG	720	
DB	661	CCCAATGACTTGTGGGTGTGTTCCAGTTTCACACATCATGCTGCTTATCTCG	720	
QY	721	CCGGAATGTGATCTGTCCTGCTATGTCATATCATCTCCAAAGTGCACACTCCAG	780	
DB	721	CCGGAATGTGATCTGTCCTGCTATGTCATATCATCTCCAAAGTGCACACTCCAG	780	
QY	781	GGCCACCAAGAGGCAAGGCGCTCAAGACACAGTATCTCTCTGCTTCTTCGCGC	840	
DB	781	GGCCACCAAGAGGCAAGGCGCTCAAGACACAGTATCTCTCTGCTTCTTCGCGC	840	
QY	841	TGTGGCTGCTTACTACATTTGGGATGACATGACTCTCTTCACTCTCTGGAAATCAGC	900	
DB	841	TGTGGCTGCTTACTACATTTGGGATGACATGACTCTCTTCACTCTCTGGAAATCAGC	900	
QY	901	AAGCAAGGGGTGAGTTTGAGACATGTGCACATGATGATTCATACCGGAGCCCA	960	
DB	901	AAGCAAGGGGTGAGTTTGAGACATGTGCACATGATGATTCATACCGGAGCCCA	960	
QY	961	GCTTCTTCACATGTTGTGGAACCCCATCTCTATCTCTTCTGAGACCAATTTAA	1020	
DB	961	GCTTCTTCACATGTTGTGGAACCCCATCTCTATCTCTTCTGAGACCAATTTAA	1020	
QY	1021	ACCTTGCCAGCAGCACTACCTCTGTGAGAGAGGGTCCAGCTCAAGATCTCTCC	1080	
DB	1021	ACCTTGCCAGCAGCACTACCTCTGTGAGAGAGGGTCCAGCTCAAGATCTCTCC	1080	

QY	1081	AAAGGAAGCGAGGTGACATTCATCTGTTCCACTGAGTGCAGTCAAGTTTTCAC	1140	
DB	1081	AAAGGAAGCGAGGTGACATTCATCTGTTCCACTGAGTGCAGTCAAGTTTTCAC	1140	
QY	1141	TCCAGCTAACACAGATGTAAAGACTTTTATATAGATTAATTAAGTTTAAATT	1200	
DB	1141	TCCAGCTAACACAGATGTAAAGACTTTTATATAGATTAATTAAGTTTAAATT	1200	
QY	1201	ACACATTTTACAGATATTAAGACTGACCAATATTGACAGTTTATGCTGTGGAT	1260	
DB	1201	ACACATTTTACAGATATTAAGACTGACCAATATTGACAGTTTATGCTGTGGAT	1260	
QY	1261	TTTGTCTGTTGTTCTTATGTTTGAAGTTAATATGCTATTAATTAATTTT	1320	
DB	1261	TTTGTCTGTTGTTCTTATGTTTGAAGTTAATATGCTATTAATTAATTTT	1320	
QY	1321	TTTGTCTATATGATGTTGTTAGGAGACCTGTGGCCAGTTCTTATGCTGTAT	1380	
DB	1321	TTTGTCTATATGATGTTGTTAGGAGACCTGTGGCCAGTTCTTATGCTGTAT	1380	
QY	1381	GTTCTGTTGTTGAGCTGTAGAAAAGGAACTGAACATTTCCAGACCTGTAGTACG	1440	
DB	1381	GTTCTGTTGTTGAGCTGTAGAAAAGGAACTGAACATTTCCAGACCTGTAGTACG	1440	
QY	1441	TAAAGCTGAATATGATCCCGAGCTGTTATGATAGATTAATCTCCATTCGCTGAC	1500	
DB	1441	TAAAGCTGAATATGATCCCGAGCTGTTATGATAGATTAATCTCCATTCGCTGAC	1500	
QY	1501	GTTTTCTGTTCTTAAGACGTGATTTTCTGTAGAAAGTGGCACTTAACAAAGCCC	1560	
DB	1501	GTTTTCTGTTCTTAAGACGTGATTTTCTGTAGAAAGTGGCACTTAACAAAGCCC	1560	
QY	1561	AAAGTGTATGAATATGCTGTTTTCAGTTTGAAGAGTGGGTTGATTACGACCTAC	1620	
DB	1561	AAAGTGTATGAATATGCTGTTTTCAGTTTGAAGAGTGGGTTGATTACGACCTAC	1620	
QY	1621	AGTGTACAGCTCTGTATTAAGTTGTTAATAAGATGTTAATTAAGTTAATAA	1680	
DB	1621	AGTGTACAGCTCTGTATTAAGTTGTTAATAAGATGTTAATTAAGTTAATAA	1680	
QY	1681	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCAGCACACTGGAATTC	1737	
DB	1681	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCAGCACACTGGAATTC	1737	

RESULT 4

ID	X15882	standard; cDNA; 1944 BP.
AC	X15882:	
DT	12-MAY-1999	(first entry)
DE	cDNA encoding G-protein coupled receptor polypeptide designated CXCR4B.	
KM	G-protein coupled receptor; CXCR4B; human; splice variant;	
KM	chemokine receptor; CXCR4; vaccine; gene therapy; HIV-1; HIV-1;	
KM	cancer; pain; diabetes; obesity; anorexia; bulimia; asthma;	
KM	Parkinson's disease; acute heart failure; hypotension; hypertension;	
KM	urinary retention; osteoporosis; angina pectoris; myocardial infarction;	
KM	stroke; ulcer; allergy; benign prostatic hypertrophy; migraine;	
KM	vomiting; psychotic disorder; neurological disorder; anxiety;	
KM	schizophrenia; manic depression; delirium; dementia; mental retardation;	
KM	dyskinesias; Huntington's disease; Gilles de la Tourette syndrome; ss.	
OS	Homo sapiens.	
FN	Key	Location/Qualifiers
FT	CDS	336..1406
FT		/*tag- a
FT	misc-feature	361
FT		/*tag- b
FT		/note- "splice acceptor site"
PD	EP-897980-42.	
PD	24-FEB-1999.	
PD	07-AUG-1998.	306324.
PR	24-JUL-1998;	US-056601.
PR	20-AUG-1997;	US-056601.

PA (SMIX) SMITHKLINE BEECHAM CORP.
PI Gupta SK, Pillariseti K;
DR WPI: 99-134643/12.
P-PSDB: W97362.
PT New G protein coupled receptor (CXCR4B) polypeptide and
PT polynucleotide, human splice variant of a chemokine receptor -
PT useful as diagnostic reagents and for prevention and treatment of
PT HIV infection, cancer, stroke and dementia
PS Claim 2: Page 16-17; 24pp; English.
CC The present sequence encodes a G-protein coupled receptor polypeptide
CC designated CXCR4B, which is a human splice variant of a chemokine
CC receptor CXCR4. CXCR4B polynucleotides and polypeptides are useful for
CC diagnosing susceptibility to diseases by detecting mutations or
CC polymorphisms in the CXCR4B gene or analysing for the presence or amount
CC of CXCR4B polypeptide expressed in a patient. CXCR4B polypeptides and
CC polynucleotides are also useful for screening for antagonists and
CC agonists which can be used to treat conditions associated with CXCR4B
CC polypeptide imbalance. CXCR4B polypeptides can be administered directly
CC (as a vaccine) or via a vector (gene therapy) to prevent disease.
CC Diseases diagnosed, prevented and treated include: HIV-1 and HIV-1
CC infections; cancer; pain; diabetes; obesity; anorexia; bulimia; asthma;
CC Parkinson's disease; acute heart failure; hypotension; hypertension;
CC urinary retention; osteoporosis; angina pectoris; myocardial infarction;
CC stroke; ulcers; allergies; benign prostatic hypertrophy; migraine;
CC vomiting; psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia and severe mental
CC retardation; and dyskinesias, such as Huntington's disease or Gilles de
CC La Tourette syndrome. CXCR4B polypeptides are useful for mapping genes
CC to chromosomes, allowing gene inheritance to be studied through linkage
CC analysis.
SQ Sequence 1944 BP; 497 A; 437 C; 412 G; 596 T;

Query Match 90.3%; Score 1569.2; DB 1; Length 1944;
Best Local Similarity 99.8%; Pred. No. 3e-282;
Matches 1579; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 106 ATATCACTCGATACATACACCGAGAAATGGGCTCGGGGACATACATCCATGANG 165
DB 363 ATATCACTCGATACATACACCGAGAAATGGGCTCGGGGACATACATCCATGANG 422
QY 166 GAACCCCTGTTCCGTGAAGAAAATGCTAATTTCAATAAATCTCTGCCACCATCTAC 225
DB 423 GAACCCCTGTTCCGTGAAGAAAATGCTAATTTCAATAAATCTCTGCCACCATCTAC 482
QY 226 TCCATCATCTTTTAACTGACATTGTGGCAATGATTTGCTATCCTGGTCAATGGTTAC 285
DB 483 TCCATCATCTTTTAACTGACATTGTGGCAATGATTTGCTATCCTGGTCAATGGTTAC 542
QY 286 CAGAAGAACTGAGAGACTGACGGACAGTAGAGGCTCAGCTGATGAGCCGACACCTC 345
DB 543 CAGAAGAACTGAGAGACTGACGGACAGTAGAGGCTCAGCTGATGAGCCGACACCTC 602
QY 346 CTCCTTGTATCAGCGCTTCCCTTGTGGGAGTTGATGCCGTGGCAAACTGTACTTTGGG 405
DB 603 CTCCTTGTATCAGCGCTTCCCTTGTGGGAGTTGATGCCGTGGCAAACTGTACTTTGGG 662
QY 406 AACTTCCATGGAAGGACAGTGCATGCTACACAGTCAACCTCTACAGCAGTGTCTTC 465
DB 663 AACTTCCATGGAAGGACAGTGCATGCTACACAGTCAACCTCTACAGCAGTGTCTTC 722
QY 466 ATCCGTGGCTTCATAGCTGAGCGCTACCTGAGCATGCTCAGCGCCACCAAGAGTGA 525
DB 723 ATCCGTGGCTTCATAGCTGAGCGCTACCTGAGCATGCTCAGCGCCACCAAGAGTGA 782
QY 526 AGGCCAAGAACCTGTGGCTGAAGAAAGTGCTATGTGGGCTGTGATCCCTGCCCTC 585
DB 783 AGGCCAAGAACCTGTGGCTGAAGAAAGTGCTATGTGGGCTGTGATCCCTGCCCTC 842
QY 586 CTGCTGACTATTCGGAGACTCATCTTTGGCAAGCTCAGTGAGGAGAGATGACATATATC 645
DB 843 CTGCTGACTATTCGGAGACTCATCTTTGGCAAGCTCAGTGAGGAGATGACATATATC 902

QY 646 TGTGACCCGCTTTACCCCAATGACTTTGGGGTGTGTTGTTCCAGTTCCAGCATATG 705
DB 903 TGTGACCCGCTTTACCCCAATGACTTTGGGGTGTGTTGTTCCAGTTCCAGCATATG 962
QY 706 GTTGGGCTTATCCGCGTATTTGTCATCCGCTCCTGATTTGATATATATCTCCAG 765
DB 963 GTTGGGCTTATCCGCGTATTTGTCATCCGCTCCTGATTTGATATATATCTCCAG 1022
QY 766 CTGTACACCTCCAAAGGCGCCACAGAGGCGCAAGGCGCTCAAGACCATCTCTCATC 825
DB 1023 CTGTACACCTCCAAAGGCGCCACAGAGGCGCAAGGCGCTCAAGACCATCTCTCATC 1082
QY 826 CTGGCTTTCTTGCTGCTTTGGCTGCTTACTACATTTGAGATCAGATGACTCTTATC 885
DB 1083 CTGGCTTTCTTGCTGCTTTGGCTGCTTACTACATTTGAGATCAGATGACTCTTATC 1142
QY 886 CTCCGGAATATACAGAGGAGTGTGATTTGGAACACTGTGCACAGTGGATTTCC 945
DB 1143 CTCCGGAATATATACAGAGGAGTGTGATTTGGAACACTGTGCACAGTGGATTTCC 1202
QY 946 ATACCCGAGGCGCTTCTTCCACTGTTGTCTGAACCCCATCCTATGCTTCTCT 1005
DB 1203 ATACCCGAGGCGCTTCTTCCACTGTTGTCTGAACCCCATCCTATGCTTCTCT 1262
QY 1006 GGAGCCAAATTTAAACTCTGCGCCAGCAGCAGTCACTCCTCTGTGACAGAGGCTCCAGC 1065
DB 1263 GGAGCCAAATTTAAACTCTGCGCCAGCAGCAGTCACTCCTCTGTGACAGAGGCTCCAGC 1322
QY 1066 CTCAGATCTCTCCAAAGAAAGGAGGTGACATTCATCTGTTCCACGAGTCTGAG 1125
DB 1323 CTCAGATCTCTCTCCAAAGAAAGGAGGTGACATTCATCTGTTCCACGAGTCTGAG 1382
QY 1126 TCTTCAAGTTTCACTCAGCTACACAGATGTAAAGACTTTTATATACGATATAA 1185
DB 1383 TCTTCAAGTTTCACTCAGCTACACAGATGTAAAGACTTTTATATACGATATAA 1442
QY 1186 ACTTTTATTAAGTATACATTTTTCATATATAAAGACTGACCAATTTGACAGTTT 1245
DB 1443 ACTTTTATTAAGTATACATTTTTCATATATAAAGACTGACCAATTTGACAGTTT 1502
QY 1246 TATTCCTGTTGGATTTTGTCTGTTGTTCTTGAATTTGTAAGTTAATGACTTA 1305
DB 1503 TATTCCTGTTGGATTTTGTCTGTTGTTCTTGAATTTGTAAGTTAATGACTTA 1562
QY 1306 TTTATATATAATTTTGTGTTTCATATGATGTGTCTAGCAGACCTGTGCCAAGT 1365
DB 1563 TTTATATATAATTTTGTGTTTCATATGATGTGTCTAGCAGACCTGTGCCAAGT 1622
QY 1366 TCTTAGTGTGATGCTGCTCGGTAGAGACTGTAAAGGAACCTGAAATTCAGAGC 1425
DB 1623 TCTTAGTGTGATGCTGCTCGGTAGAGACTGTAAAGGAACCTGAAATTCAGAGC 1682
QY 1426 GTGTAGATACAGCTAAAGCTAGAAATGATCCAGCTGTTATGCAATGATATCTCT 1485
DB 1683 GTGTAGATACAGCTAAAGCTAGAAATGATCCAGCTGTTATGCAATGATATCTCT 1742
QY 1486 CCATTCGCCGTGAGACGTTTCTCTGTTTAAAGAGCTATTTTGTGTGAAGATGACAC 1545
DB 1743 CCATTCGCCGTGAGACGTTTCTCTGTTTAAAGAGCTATTTTGTGTGAAGATGACAC 1802
QY 1546 TTATATACCAAGGCCAAAGTGTATAGAAATGCTGTTTCAAGTTTCCAGAGTGGGT 1605
DB 1803 TTATATACCAAGGCCAAAGTGTATAGAAATGCTGTTTCAAGTTTCCAGAGTGGGT 1862
QY 1606 GATTTACAGCTACAGTGTAC - ACTCTGTATTAAGTTGTTAAATTAAGTACATGTTAA 1664
DB 1863 GATTTACAGCTACAGTGTACAGTGTGATTAAGTTGTTAAATTAAGTACATGTTAA 1922
QY 1665 ACTTAAAAAAAAAAAAAAAAAAAA 1686
DB 1923 ACTTAAAAAAAAAAAAAAAAAAAA 1944

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RESULT 5
V18357
ID V18357 standard; DNA: 1317 BP.
AC V18357;
DE 25-SEP-1998 (first entry)
KW Human RM3 seven transmembrane (7TM) receptor cDNA.
KW V28: Placenta; seven transmembrane receptor; 7TM: signal transduction;
OS Immunology; inflammation; RM3; SS.
FH Homo sapiens.
FT Key Location/Qualifiers
FT CDS 201..1211
FT /tag= a
FT /product= "Human RM3 seven transmembrane receptor"
PD US759804-A.
PD 02-JUN-1998.
PD 17-NOV-1993; 153848.
PD 17-NOV-1992; US-977452.
PA (ICOS-) ICOS CORP.
PI Godiska R, Gray PW, Schweickart VL;
PI WPI; 98-332132/29.
DR P-PSDB: W48734.
DR WPI: 98-332132/29.
PT DNA encoding V28 seven transmembrane receptor polypeptide - useful
PT for producing recombinant polypeptide and anti-V28 antibodies, and
PT in screening assays for V28 agonists and antagonists
PS Example 11; Columns 89-94; 56BP; English.
CC The present novel sequence represents the human RM3 cDNA, isolated
CC from a human macrophage cDNA library. The invention claims for
CC the full length V28 genomic DNA sequence (V18343) isolated from a human
CC placenta genomic library. The V28 (W48722) and RM3 proteins are seven
CC transmembrane (7TM) receptors which are probably involved in signal
CC transduction. The invention also claims that cells transformed with
CC V28 DNA can be used to produce the recombinant polypeptide, to produce
CC anti-V28 antibodies or in screening assays for V28 agonists or
CC antagonists. The antibodies, agonists and antagonists could then be
CC used to modulate V28 receptor-ligand binding, for e.g. in immunological
CC and/or inflammatory events in vivo.
SQ Sequence 1317 BP; 332 A; 342 C; 265 G; 378 T;

Query Match 64.4%; Score 1118.2; DB 1; Length 1317;
Best Local Similarity 99.6%; Pred. No. 8,4e-199;
Matches 1131; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 106 ATATACATTCAGATACTACACCGAGAAATGGGCTCAGGAGATGATGATCCATGTAAG 165
DB 171 ATATACATTCAGATACTACACCGAGAAATGGGCTCAGGAGATGATGATCCATGTAAG 230
QY 166 GAACCCGTTTCGGTGAAAGAAATGCTAATTCAATTAATCTTCTGCCACCATCTAC 225
DB 231 GAACCCGTTTCGGTGAAAGAAATGCTAATTCAATTAATCTTCTGCCACCATCTAC 290
QY 226 TCCATCATCTTCTTAATGATGATGAGGATGATGATGATGATGATGATGATGATGATG 285
DB 291 TCCATCATCTTCTTAATGATGATGAGGATGATGATGATGATGATGATGATGATGATG 350
QY 286 CAGAGAACTGAGAGCATGACGAGCAAGTACAGGCTGACCTGCTCAAGTGGCCGACCTC 345
DB 351 CAGAGAACTGAGAGCATGACGAGCAAGTACAGGCTGACCTGCTCAAGTGGCCGACCTC 410
QY 346 CTCTTGATCATCGGCTCCCTCTGCGAGTGTGAGTGGCGGCAAGTGTGATCTTTGGG 405
DB 411 CTCTTGATCATCGGCTCCCTCTGCGAGTGTGAGTGGCGGCAAGTGTGATCTTTGGG 470
QY 406 AACTTCCATGCAAGGAGTGCATGCTATCTACAGTCAAGTCAAGTCAAGTCAAGTCAAG 465
DB 471 AACTTCCATGCAAGGAGTGCATGCTATCTACAGTCAAGTCAAGTCAAGTCAAGTCAAG 530
QY 466 ATCTTGCCCTTATCATGCTGAGCCGCTACCTGGCCATGCTCCAGCCCAACAGTCAAG 525
DB 531 ATCTTGCCCTTATCATGCTGAGCCGCTACCTGGCCATGCTCCAGCCCAACAGTCAAG 590
QY 526 AGGCCAAGGAAGCTGTGGCTGAAGAGTGCTATGTTGGGCTGTGATCCCTGCTC 585
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DB 591 AGGCCAAGGAAGCTGTGGCTGAAGAGTGCTATGTTGGGCTGTGATCCCTGCTC 650
QY 586 CTGCTAGTATTCGCCAGTCACTCTTTGGCAACGTCAGTGAAGGAGATGACAGATATTC 645
DB 651 CTCTACTATTCGCCAGTCACTCTTTGGCAACGTCAGTGAAGGAGATGACAGATATTC 710
QY 646 TGTGACCGCTTACCCCAATGACTGTGGGTGGTGTGTTGTTGTCAGTTCAGACATCATG 705
DB 711 TGTGACCGCTTACCCCAATGACTGTGGGTGGTGTGTTGTTGTCAGTTCAGACATCATG 770
QY 706 GTTGGCCCTTATCCTGCTGTGATGTTGATCCTGCTGCTATGCTATGATATCTCCAA 765
DB 771 GTTGGCCCTTATCCTGCTGTGATGTTGATCCTGCTGCTATGCTATGATATCTCCAA 830
QY 766 CTGTCACTCAAGGAGGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 825
DB 831 CTGTCACTCAAGGAGGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 890
QY 826 CTGGCTTCTTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 885
DB 891 CTGGCTTCTTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 950
QY 886 CTCTGGAATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 945
DB 951 CTCTGGAATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1010
QY 946 ATACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1005
DB 1011 ATACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1070
QY 1006 GGAGCCAAATTTAAACTCTGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1065
DB 1071 GGAGCCAAATTTAAACTCTGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1130
QY 1066 CTCAGATCTCTCTCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1125
DB 1131 CTCAGATCTCTCTCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1190
QY 1126 TCTTAAAGTTCACCTCAGCTTAACAGATGTAAGAGCTTTTATATGATTAATA 1185
DB 1191 TCTTAAAGTTCACCTCAGCTTAACAGATGTAAGAGCTTTTATATGATTAATA 1249
QY 1186 ACTTTTAAAGTTCACCTTTCAGATTAATAAGCTGACCAATATGTTGATA 1240
DB 1250 ACTTTTAAAGTTCACCTTTCAGATTAATAAGCTGACCAATATGTTGATA 1304

RESULT 6
066179
ID 066179 standard; cDNA: 1317 BP.
AC 066179;
DE 07-FEB-1995 (first entry)
DE Seven transmembrane receptor (RM3) coding sequence.
KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
KW Polymerase chain reaction; ss.
FH Homo sapiens.
FT Key Location/Qualifiers
FT CDS 201..1214
FT /tag= a
FT /product= "Seven transmembrane receptor"
PD M09412635-A.
PD 09-JUN-1994.
PD 17-NOV-1993; U11153.
PD 17-NOV-1992; US-977452.
PA (ICOS-) ICOS CORP.
PI Godiska R, Gray PW, Schweickart VL;
PI WPI; 94-200264/24.
DR P-PSDB: R53753.
DR WPI: 94-200264/24.
PT DNA encoding seven transmembrane receptors - used to develop
PT prods. for use as therapeutic or diagnostic agents for conditions
PT involving the receptors.
PS Example 11; Page 82-83; 100BP; English.
CC Two primers (066148, 066149) were used in a PCR reaction containing
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CC human macrophage cDNA library in plasmid pRC/CMV. When the PCR
CC products were subjected to agarose gel electrophoresis a faint band
CC of 180-200 base pairs was observed. Re-amplified material was
CC digested with BamHI and HindIII and cloned into the plasmid
CC Bluescript SK-. Of sixteen clones sequenced, two contained a unique
CC sequence termed RM3. Specific primers for the partial RM3 clone were
CC used to identify this full length RM3 cDNA clone.
50 Sequence 1317 BP: 332 A: 343 C: 264 G: 378 T:

5Q Sequence 1317 BP; 332 A; 343 C; 264 G; 378 T;

Query Match	64.3%	Score	1116.6	-DB 1	Length	1317
Best Local Similarity	99.6%	Pred. No.	1.7e-198			
Matches 1130	Conservative	0	Mismatches	4	Indels	1
					Gaps	1

QY	106	ATAATACCTTCAAGTAATCACTACACCGAGAAATGGGCTACAGGGACTATGATCTCATGAAG	165
Db	171	ATATACACTTCAAGTAATCACTACACCGAGAAATGGGCTACAGGGACTATGATCTCATGAAG	230
QY	166	GAACCCGTGTTCCGTGAGAAAATGCTAATTCAATPAAAATCTTCTCGCCACCATCTAC	225
Db	231	GAACCCGTGTTCCGTGAGAAAATGCTAATTCAATPAAAATCTTCTCGCCACCATCTAC	290
QY	226	TCACATCACTTCTTAATCTGCAATGTGSGGCAATGGAATGGTCAATCCTGGTCAATGGGTTAC	285
Db	291	TCACATCACTTCTTAATCTGCAATGTGSGGCAATGGAATGGTCAATCCTGGTCAATGGGTTAC	350
QY	286	CAGAAGAACTGAGAAAGCATGACGGAGCAAGTACAGGCTGACCTGTCACTGGGCGCACTAC	345
Db	351	CAGAAGAACTGAGAAAGCATGACGGAGCAAGTACAGGCTGACCTGTCACTGGGCGCACTAC	410
QY	346	CTCTTTGTCAACAGCTTCCCTTCTGGGCAAGTTGATGCGGTGGCAAACTGTACTTTGGG	405
Db	411	CTCTTTGTCAACAGCTTCCCTTCTGGGCAAGTTGATGCGGTGGCAAACTGTACTTTGGG	470
QY	406	AACCTCTATGCAAGGACGATCCATGTATATACAGATCAACCTGTACAGCAAGTGTCCAC	465
Db	471	AACCTCTATGCAAGGACGATCCATGTATATACAGATCAACCTGTACAGCAAGTGTCCAC	530
QY	466	ATCTGGCCCTTCACTCACTGTGACACCGCTACCTGGCCATGCTGCACGCCAACCAACAGTCAG	525
Db	531	ATCTGGCCCTTCACTCACTGTGACACCGCTACCTGGCCATGCTGCACGCCAACCAACAGTCAG	590
QY	526	AGGCGCAAGGAAGCTGTGGCTGAAAAGGATGTATATGTTGGGCTGTGAAATCCCTGGCCCTC	585
Db	591	AGGCGCAAGGAAGCTGTGGCTGAAAAGGATGTATATGTTGGGCTGTGAAATCCCTGGCCCTC	650
QY	586	CTGCTGACTATTCGCGACTTCATCTTTGGCCACAGTACAGTAGGAGCAGATACAGATATATAC	645
Db	651	CTGCTGACTATTCGCGACTTCATCTTTGGCCACAGTACAGTAGGAGCAGATACAGATATATAC	710
QY	646	TGTGACCGCTTTCACCCCAATGACTGTGTGGGTGTTGTGTCTCAGTTTAGACATCATATG	705
Db	711	TGTGACCGCTTTCACCCCAATGACTGTGTGGGTGTTGTGTCTCAGTTTAGACATCATATG	770
QY	706	GTTGCGCTTATCTGTGCTGTGATTTGTTCATCTCTCGTATTTGACATATACATCTCCAAAG	765
Db	771	GTTGCGCTTATCTGTGCTGTGATTTGTTCATCTCTCGTATTTGACATATACATCTCCAAAG	830
QY	766	CTGTCACTATCCAAAGGGCCACCCAGAAAGCCAGAGGCCCTCAAGACCAAGCTCATCTCTATC	825
Db	831	CTGTCACTATCCAAAGGGCCACCCAGAAAGCCAGAGGCCCTCAAGACCAAGCTCATCTCTATC	890
QY	826	CTGCGTTTCTTGCGCTTGTGGTGGCTTACTATTAATTGGGATCGAATGACATCTTCATC	885
Db	891	CTGCGTTTCTTGCGCTTGTGGTGGCTTACTATTAATTGGGATCGAATGACATCTTCATC	950
QY	886	CTCTCGAAAAATCATCAAGCAAGGGTGTGACTTTGAGAAACCTGTGACCAAGTGGATTTC	945
Db	951	CTCTCGAAAAATCATCAAGCAAGGGTGTGACTTTGAGAAACCTGTGACCAAGTGGATTTC	1011
QY	946	ATACACGAGGCGCTAGCTTTCTTCACACTGTGTTGCTGAACCCATCCTCATGCTTTCTCT	1005
Db	1011	ATACACGAGGCGCTAGCTTTCTTCACACTGTGTTGCTGAACCCATCCTCATGCTTTCTCT	1070

QY	1006	GGAGCCAAATTTAAACCTCTGGCCAGCAGCAGCACTACCTCTGTAGCAGAGGGTCCAGC	1065
QY	1006	GGAGCCAAATTTAAACCTCTGGCCAGCAGCAGCACTACCTCTGTAGCAGAGGGTCCAGC	1065
Db	1071	GGAGCCAAATTTAAACCTCTGGCCAGCAGCAGCACTACCTCTGTAGCAGAGGGTCCAGC	1130
QY	1066	CTCAAGATCCTCTCCAAAGGAAAGCGAGGTGCACATTCATCTGTTTCCACTGAGTCTGAG	11235
Db	1131	CTCAAGATCCTCTCCAAAGGAAAGCGAGGTGCACATTCATCTGTTTCCACTGAGTCTGAG	1130
QY	1126	TCTTCAGTCTTTCACCTCCAGCTAACACACATGTGAAAAAGCACTTTTTRTACGATTAATA	1185
Db	1191	TCTTCAGTCTTTCACCTCCAGCTAACACACATGTGAAAAAGC -TTTTTTTATAGATTAATA	1249
QY	1186	ACTTTTAAAAAGTACACACTTTTTCAGATATTAAGACGTGACCAATATTGTACA	1240
Db	1250	ACCTTTTAAAAAGTACACACTTTTTCAGATATTAAGACGTGACCAATATTGTAAAA	1304

RESULT	7
ID	V46370 standard; cDNA to mRNA; 1877 BP.
DC	V46370; 1998 (first entry)
DE	Nucleic acid encoding a murine CXc chemokine receptor.
KW	Mouse; CXc chemokine receptor; pre-B cell line DM34;
KW	CXc chemokine pre-B cell stimulatory factor PSF/SDF-1;
KW	HIV infection; screening; inhibitor; AIDS; ds.
OS	Mus sp.
FX	Location/Qualifiers
FT	120..1199
FT	/*tag- a
PN	W09835035-A1.
PD	13-AUG-1998.
PF	07-FEB-1997; J00299.
PR	07-FEB-1997; WO-J00299.
RA	(SHIO) SHIONOGI & CO LTD.
P1	Ilasa H, Kishimoto T, Nagasawa T, Nakajima T, Tachibana K,
P1	Yoshida N, Yoshie O;
DR	WPI: 98-447232/38.
DR	P-PSDB: W64778.
PT	Mouse CXc chemokine receptor binding to PSF/SDF-1 pre-B cell
PT	stimulatory factor - is useful for screening of potential HIV
PT	infection and AIDS inhibitors
PS	Claim 3; Pages 39-42; 76pp; Japanese.
CC	The present sequence encodes a murine CXc chemokine receptor which
CC	binds to the mouse CXc chemokine pre-B cell stimulatory factor
CC	PSF/SDF-1. The nucleic acid is isolated from mouse pre-B cell
CC	line DM34. The receptor and cells expressing it can be used in the
CC	study and mapping of the mechanism of HIV infection and in screening
CC	of potential inhibitors of HIV infection and the development of AIDS
Sequence	1877 BP: 469 A: 451 C: 406 G: 551 T:

Query Match	56.1%	Score 974.4	DB 1	Length 1877
Best Local Similarity	76.1%	Pred. No. 3	7e-172	
Matches 1391, Conservative	0	Mismatches 301	Indels 136	Gaps 10

QY	20	GC	GGGGCCCAAA	AG	TGACG	CCGACGGG	CCCTG	AGT	GTCTCC	AGT	TGACCG	CAACCG	CACT	TGSGA	AGAC	79
Db	50	GC	AGGTACCACT	GTGACC	CTCTG	TGAGGCG	CTTTGGT	TGCTCC	GGTAC	CCACCA	CGCGCT	TGTAA	GCG			105
QY	80	C	AGCGGTACCAT	TGAG	-----	G	GGGAT	CAGAT	ATAT	TAC	ACTTC	CAGAT	TACT	ATAC	CCGAG	134
Db	110	G	AGTGTTC	CCCAT	TGGA	ACC	CGAT	CA	GTG	AGAT	ATAT	TAC	ACTT	CT	TATAT	165
QY	135	A	ATGGGCT	CAG	GGGAC	TATG	ACT	TGC	ATG	AA	GAA	ACC	TGTT	CCG	TGA	194
Db	170	A	GTGGGGCT	GTG	AACT	ATG	ACT	CTCA	CA	AA	GAA	ACC	TGCT	CCG	GAT	228
QY	195	T	TTC	AA	TAA	AT	CT	TCT	G	CC	CA	CACT	TACT	CA	TAT	254
Db	230	T	TTC	AA	TAA	AT	CT	TCT	G	CC	CA	CACT	TACT	CA	TAT	289

CC agonists which can be used to treat conditions associated with CXCR4B
CC polypeptide imbalance. CXCR4B polypeptides can be administered directly
CC (as a vaccine) or via a vector (gene therapy) to prevent disease.
CC Diseases diagnosed, prevented and treated include: HIV-1 and HIV-1
CC infections; cancer; pain; diabetes; obesity; anorexia; bulimia; asthma;
CC Parkinson's disease; acute heart failure; hypotension; hypertension;
CC urinary retention; osteoporosis; angina pectoris; myocardial infarction;
CC stroke; ulcers; allergies; benign prostatic hypertrophy; migraine;
CC vomiting; psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia and severe mental
CC retardation; and dyskinesias, such as Huntingtons disease or Gilles de
CC la Tourette syndrome. CXCR4B polypeptides are useful for mapping genes
CC to chromosomes, allowing gene inheritance to be studied through linkage
CC analysis.
SQ Sequence 611 BP: 166 A: 125 C: 139 G: 181 T;

Query Match 14.3%; Score 249; DB 1; Length 611;
Best Local Similarity 100.0%; Pred. No. 5.6e-38;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 ATATACCTTACATACACACGAGAAATGGCTCAGGGAGCTATGACTCCATGAAG 165
DB 363 ATATACCTTACATACACACGAGAAATGGCTCAGGGAGCTATGACTCCATGAAG 422

QY 166 GAACCCCTGTTCCGTGAAGAAATGCTAATTTCAATTAATAATCTTCCGCCACCATCTAC 225
DB 423 GAACCCCTGTTCCGTGAAGAAATGCTAATTTCAATTAATAATCTTCCGCCACCATCTAC 482

QY 226 TCCATCATCTTCTTAACTGCGATGTGGCAATGATTGGTCATCTCGTCATGGGTTAC 285
DB 483 TCCATCATCTTCTTAACTGCGATGTGGCAATGATTGGTCATCTCGTCATGGGTTAC 542

QY 286 CAGAGAACTGAGACATGACGAGCAAGTACAGCTGCACCTGTCAGTGGCGACCTC 345
DB 543 CAGAGAACTGAGAGAACATGACGAGCAAGTACAGCTGCACCTGTCAGTGGCGACCTC 602

QY 346 CTCTTTGTC 354
DB 603 CTCTTTGTC 611

RESULT 9
T20146
ID T20146 standard: cDNA to mRNA: 218 BP.
AC T20146:
DT 31-JUL-1996 (first entry)
DE Human gene signature HUMGS01292.
KM Gene signature; messenger RNA; mRNA: relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
OS Homo sapiens.
PI WO9514772-A1.
PD 01-JUN-1995.
PR 11-NOV-1994; J01916.
PR 12-NOV-1993; JP-355504.
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
PI Matsubara K, Okubo K;
DR WPI: 95-20631/27.
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
PS Claim 1: Page 571-572: 2245pp; Japanese.
CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in T19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost

CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
SQ Sequence 218 BP: 61 A: 38 C: 44 G: 75 T;

Query Match 12.6%; Score 218; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.5e-32;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1454 GATCCGACGTGTTATGATAGATATCTCTCCATCCGTGAGAGCTTTTCCGTTC 1513
DB 1 GATCCGACGTGTTATGATAGATATCTCTCCATCCGTGAGAGCTTTTCCGTTC 60

QY 1514 TTAGAGCTATTTTGGTGTGAGAGATGCGACTATATACCAAGCCAAAGTGATAGA 1573
DB 61 TTAGAGCTATTTTGGTGTGAGAGATGCGACTATATACCAAGCCAAAGTGATAGA 120

QY 1574 AATGCTGTTTTCAGTTTCAGAGATGGGTGATTTTCAGACACTACAGTGTACGTCTT 1633
DB 121 AATGCTGTTTTCAGTTTTCAGAGATGGGTGATTTTCAGACACTACAGTGTACGTCTT 180

QY 1634 GTATTAAAGTTGTTAATAAAGTACATGTAACTTAA 1671
DB 181 GTATTAAAGTTGTTAATAAAGTACATGTAACTTAA 218

RESULT 10
Q30011
ID Q30011 standard: cDNA: 1200 BP.
AC Q30011:
DT 04-APR-1993 (first entry)
DE Sequence encoding a high affinity recombinant rabbit Interleukin-8
DE (IL-8) receptor polypeptide in F3R.
KM IL-8 receptor polypeptide; G-protein-coupled receptor; ss.
OS Oryctolagus cuniculus.
FH key location/Qualifiers
FT cds 108..1172
PN WO9218641-A.
PD 29-OCT-1992.
PE 10-APR-1992; 002977.
PR 10-APR-1991; US-685101.
PR 09-JUL-1991; US-726606.
PR 09-DEC-1991; US-803842.
PA (REPK) REPLIGEN CORP.
PA (UYBO-) UNIV BOSTON.
PI Navarro J, Thomas KM, Wilt DP;
DR WPI: 92-382123/46.
DR P-PSDB: R28272.
PT Recombinant mammalian interleukin-8 receptor - used for screening
PT interleukin-8 binding antagonists, used to treat inflammation
PS Disclosure, Fig 1: 74pp; English.
CC Rabbit high affinity IL-8 receptor gene was isolated from rabbit
CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
CC plaques were screened for those which hybridized to an antisense
CC oligonucleotide (Q30015). This probe was designed based on the
CC sequence derived from the second transmembrane domain of G-protein-
CC coupled receptors. After tertiary screening, six plaques were
CC isolated. The insert of one of these plaques, termed F3R was of 2.5
CC kb in size. This insert was sequenced. The protein deduced from
CC the F3R clone demonstrates that it belongs to the family of
CC G-protein-coupled receptors. The deduced protein sequence
CC indicates seven putative transmembrane segments.
SQ Sequence 1200 BP: 234 A: 366 C: 294 G: 304 T;

Query Match 11.9%; Score 206.8; DB 1; Length 1200;

Best Local Similarity 54.9%; Pred. No. 4.1e-30;
Matches 456; Conservative 0; Mismatches 362; Indels 12; Gaps 2;

QY 197 TCAATAAATCTCTCTGCCCCACATCTACATCATCTCTCTTACTGAGCATGAGGCA 256
DB 232 TTAACAAATATGTTGTGTGCTGCTATGATGCTGTCTCTCTGAGCGTGGGCA 291
QY 257 ATGATGTGATCCTGCTGATGAGTGTACAGAAACTGAGATGAGCATGAGCAAGT 316
DB 292 ACTCCCTGTGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 351
QY 317 ACAGGCTGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 376
DB 352 ACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
QY 377 TTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 436
DB 412 TCTCCAGGAAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 471
QY 437 ACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 496
DB 472 AGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 531
QY 497 TGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 556
DB 532 TGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588
QY 557 TCTATGTTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616
DB 589 TATGCTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 648
QY 617 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
DB 649 AAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
QY 668 ACTGTGTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
DB 709 CGAATGTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768
QY 728 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 787
DB 769 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
QY 788 AGAAGTGTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 847
DB 829 AGAAGTGTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 888
QY 848 TGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
DB 889 TGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 948
QY 908 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 967
DB 949 CGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008
QY 968 TGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017
DB 1009 TGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1058

RESULT 11
099949
ID 099949 standard; DNA: 1200 BP.
AC 099949; (first entry)
DE Recombinant high affinity interleukin-8 receptor subtype A encoding DNA.
KW IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
systemic necrotizing vasculitis; psoriasis; asthma; allergy; ARS;
adult respiratory distress syndrome; neutrophil detection; ss.
OS Oryctolagus cuniculus.
FH key Location/Qualifiers
FT cds 108..1175

FT FT /*tag- a
FN FN /product= IL-8A_receptor
PD W09525126-A1.
PR 21-SEP-1995.
PR 09-MAR-1995; U03032.
PR 15-MAR-1994; US-210250.
PR 02-MAY-1994; US-237937.
PA (REPK) REPLIGEN CORP.
PA (UNBO-) UNIV BOSTON.
PI Greenfield EA, Larosa GJ, Navarro J, Thomas KM.
PI Wilt DT;
DR WPI: 95-336945/43.
DR P-PSDB; R80950.
PT Monoclonal antibody against recombinant IL-8 receptor polypeptide -
PT useful for treating inflammatory disorders, for detecting
PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.
PS Claim 2; Fig 1A-B; 74pp; English.
CC Monoclonal antibodies were raised against recombinant interleukin-8
CC (IL-8) receptor subtypes A and B from both human and rabbit sources
CC (R80950-53 encoded by 099949-52). The A subtype receptor (IL-8A) is
CC a high affinity receptor and the B subtype receptor (IL-8B) is a
CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
CC the IL-8 binding domain thus blocking its activation. The mAbs are
CC useful for treating inflammatory disorders (see key words) and for
CC detecting the presence of neutrophils in a biological sample. The
CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.
SQ Sequence 1200 BP; 234 A; 366 C; 295 G; 303 T;

Query Match 11.9%; Score 206.8; DB 1; Length 1200;
Best Local Similarity 54.9%; Pred. No. 4.1e-30;
Matches 456; Conservative 0; Mismatches 362; Indels 12; Gaps 2;

QY 197 TCAATAAATCTCTCTGCCCCACATCTACATCATCTCTTACTGAGCATGAGGCA 256
DB 232 TTAACAAATATGTTGTGTGCTGCTATGATGCTGTCTCTCTGAGCGTGGGCA 291
QY 257 ATGATGTGATCCTGCTGATGAGTGTACAGAAACTGAGATGAGCATGAGCAAGT 316
DB 292 ACTCCCTGTGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 351
QY 317 ACAGGCTGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 376
DB 352 ACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
QY 377 TTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 436
DB 412 TCTCCAGGAAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 471
QY 437 ACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 496
DB 472 AGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 531
QY 497 TGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 556
DB 532 TGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588
QY 557 TCTATGTTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616
DB 589 TATGCTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 648
QY 617 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
DB 649 AAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
QY 668 ACTGTGTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
DB 709 CGAATGTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768
QY 728 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 787
DB 769 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828

OY	788	AGAAAGCGCAAGGCCCTCAGACACCAGCATGTCATCCGTGGCTTTTCCGTGGGC	847
Dd	829	AGAGACCGGGGCGGCGGCGTGTCATTGGCGGTCGTGTCATCTTCTTCTGCTGGC	888
OY	848	TGCGTTACTACATTGGGATCAGCATGACGTCTTTCATCTCTCGAATAATCATCAACAAG	907
Dd	889	TGCGCTACAACTGGTGTCTCTCGAGACACCCTCATGAGAACCCAGTATCTCAGAGA	948
OY	908	GGTGTGAAGTTTGAAAACACTGTGCACAAAGTAGATTTTCATCACCGAGCCCTAGCTTCT	967
Dd	949	CCTGTACGGGTGCGCATGTGATGACCGGGCCCCTGGACGCCACCGAGATCTGGGCTTCC	1008
OY	968	TCCACTGTGTGTAAGCCCCATCCCTATGCTTTCCTTGGAGCAAATTT	1017
Dd	1009	TGCACAGCTGCTCCAACCCCATCATCATACGCCCTTCA TTGGCCAAACTTT	1058
RESULT 12			
ID	O99951	O99951 standard; DNA; 1373 BP.	
AC	O99951:		
DT	24-APR-1996	(first entry)	
DE	Recombinant high affinity interleukin-8 receptor subtype B encoding DNA,		
KM	I1-A; IL-8B: receptor; monoclonal antibody; inflammatory disorder;		
KW	anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;		
KW	systemic necrotizing vasculitis; psoriasis; asthma; allergy; ARDS;		
KW	adult respiratory distress syndrome; neutrophil detection; ss.		
OS	Oryctolagus cuniculus.		
FH	Key	location/Qualifiers	
FT	cds	/tag= a 71..1147	
ET		/product= IL-8B_receptor	
FN	WO9525126-A1.		
PD	21-SEP-1995.		
PF	09-MAR-1995: UO3032.		
PR	15-MAR-1994: US-210250.		
PR	02-MAY-1994: US-237937.		
PA	(REPK) REPLIGEN CORP.		
PI	(UYBO-) UNIV BOSTON.		
PI	Greenfield EA, Larosa GJ, Navarro J, Thomas KM;		
PI	Witt DF;		
DR	WPt: 95-336945/43.		
P-	PSDB: R80952.		
PT	Monoclonal antibody against recombinant IL-8 receptor polypeptide -		
PT	useful for treating inflammatory disorders, for detecting		
PS	neutrophil(s) and for isolating IL-8 receptor from liq.mixt.		
PC	Claim 6; Fig 3A-B: 74pp; English.		
CC	Monoclonal antibodies were raised against recombinant interleukin-8		
CC	(IL-8) receptor subtypes A and B from both human and rabbit sources		
CC	(R80950-53 encoded by Q89949-52). The A subtype receptor (IL-8ra) is		
CC	a high affinity receptor and the B subtype receptor (IL-8rb) is a		
CC	low affinity receptor. The monoclonal antibody (mAb) pref. binds to		
CC	the IL-8 binding domain thus blocking its activation. The mAbs are		
CC	useful for treating inflammatory disorders (see key words) and for		
CC	detecting the presence of neutrophils in a biological sample. The		
CC	mAbs are also useful in the isolation of IL-8 receptors from a mixture.		
SQ	Sequence 1373 BP; 266 A; 437 C; 329 G; 335 T;		
Query Match 11.6%; Score 201.2; DB 1; Length 1373; Best Local Similarity 54.8%; Pred. No. 4,6e+29; Matches 467; Conservative 0; Mismatches 373; Indels 12; Gaps 3			
OY	175	TTTCGGTGAAGAAATGCTAATTTCAATAAATCTCTGCCCCACCATCTAGCTCATCATC	234
Dd	179	TGCCCTGAGAAATCTCTGTGAAMCAACACCTATGTGTGCTCATCACTATATCTCGTGC	238
OY	235	TTCCTTAACGCGATTTGTGGCGCAATGATGTGTCATCTCGTCATGAGTTTACCAAGAA	294
Dd	239	TTCCTGCTGAGCCTGCTGGGCAACTCCCTGCTGATCTGTATCTCTGTACACCGGAGC	298
OY	295	CTGAGAGCATGACGGACAAGTACAGGCTGTGACCTGTCTAGTGGCGACCTCTCTTGTG	354

Db	299	ACCTCTCGGTGACACCGACGCTCTACCTCTGTAACCTTGCCATGCGGACCTGCTCTTTTGCC	358
Qy	355	ATCAGCGCTTCCCTCTTGCGGAGTTGATGCCGTGGCAACCTGCTACTTTGGAACTTCTTA	414
Db	359	ACCACTGTCCTTCATCTGGCGCGCTCCAAAGTGCACGGCTGGACTTTGGCACGGCCCTG	418
Qy	415	TGCAAGGACGTCATGTCATCTACACAGTCAACCTTAACAGCAGTGTCTCATCTGGCC	474
Db	419	TGTAAGGTGGTCTGGCTTGGTAAGGAAGTCACTTACACGGGAACTCTGCTCTGGCC	478
Qy	475	TTTCACTAGTGTGGACCCCTACTGAGCCATGCTGCACGGCCACCACAGTGCAGAGGCGCAAG	534
Db	479	TGCATCACTGTGGACCCGCTACTGTCATGTCTCATGCTCCACACGACAGATGATCCAGAA	538
Qy	535	AAGCTTTGGCTGAAGAGGTGTCTATGTTGGCGTGTGATCCCTGCTCCCTGCTGACT	594
Db	539	CGCCACTGG---GTCAAGTTCATATGCTTAAGCATGTGGGGAATGCTGTGATCTGCT	595
Qy	595	ATTCGCGACTCATCTTTGGCAAGCTAGTAGAGCA---GATGACAGATATATCTG---	648
Db	596	CTGCCCCATCTTACTGTTCCGTAATGCCATCTTCCACCCAAATTCAGCCCCGCTGTGCTAT	655
Qy	648	--TGACCGCTTTCACCCCAATGACTTGTGGGTGGTGTGTTCAGTTTCAGACATCAATG	705
Db	656	GAGGACATGGGGAGACACACTGCGAAATGGCGCATGTGCTGGGATCTGCTCGAGACT	715
Qy	706	GTTGGCCTTATCTGCTGCTGGTATGTCACTCTCTCTGTAATGCAATATCATCTTCCAG	765
Db	716	TTGCGCTTCACTCTGCGCGCTGTGCTATCTGTTTGGTATGTGTACCCCTGGGACAG	775
Qy	766	CTGTCACTACATCCAAAGGGCCACAGAAAGCGCAAGGCCCTCAAGACCACTCATCTCTATC	825
Db	776	CTGTTCACAGGCCCAATGGGGGCAAGAGACACCGGCCCATGGGGTCACTCTGGCGCTG	835
Qy	826	CTGGCTTTCTTCGCTCTTGGCTGTGGCTTACTTACATTTGGGATAGCATGCACTCTTTCATC	885
Db	836	CTCATCTTCTCTCTCTGTGTGGCTGCTCCATCAACCTGTGTCTGTCAACAGACCCCTCATG	895
Qy	886	CTCTCGAATATCATCAAGCAAGGGGTGGATTTGAAACACTGTGCACAAAGGATTTCC	945
Db	896	AGGACCCACGTCGATCCAGGAGACGTGTGAGCCGCCGAATGACATTTGACCGGSCCTGAC	955
Qy	946	ATCACCAGAGCCCTAGCTTTCTTCACATGTTGTGTGAAACCCCATCCTCATGCTTTTCTT	1005
Db	956	GCCACCCGAGTTTGGGCTCTCTGCAACAGTGCCTCAACCCCATCATCTAGCCCTTCAAT	1015
Qy	1006	GGAGCCAAATTT 1017	
Db	1016	GGGCAAAAGTTT 1027	
RESULT 13			
Q29505	ID	Q29505 standard; DNA; 1933 BP.	
AC	Q29505;		
DT	12-MAR-1993	(first entry)	
DE	Interleukin-8 receptor.		
KM	IL-8R; G-protein coupled receptor family; rhodopsin superfamily;		
KW	pro-inflammatory cytokine; ss.		
OS	Homo sapiens.		
PM	Key	location/Qualifiers	
FT	cds	51..1103	
FT		/*tag= a	
FT		/product= IL-8R	
PN	W09217497-A.		
PD	15-OCT-1992.		
PR	23-MAR-1992; U02317.		
PR	29-MAR-1991; US-677211.		
PR	19-DEC-1991; US-810782.		
PA	(GETH) GENENTECH INC.		
PI	Holmes WE, Lee J, Wood WI;		
DR	WPI: 92-366191/44.		
	P-PSDB: R27791.		

PT Isolated human platelet factor 4 super-family receptor
 PT polypeptide and corresp. antibodies and DNA - useful as
 PT diagnostic and screening agents, and for treating inflammation or
 PF4R-mediated disorders
 PS Claim 7: Fig 2: 78bp. English.
 CC A cDNA library constructed from human neutrophil mRNA in the mammalian
 CC expression vector pRK5B was transfected into COS-7 cells as pools of
 CC 2500 clones. One positive pool from the first 58 transfections was
 CC partitioned into smaller pools until a pure clone (pRK5B.118r1.1)
 CC was obtained. The ORF encodes a protein of 350 amino acids which
 CC shares several features with the G-protein coupled receptors of the
 CC rhodopsin superfamily, including 7 hydrophobic (transmembrane)
 CC domains. See also Q29506 and Q37107.
 CC Sequence 1933 BP; 423 A; 541 C; 483 G; 486 T;
 SO

Query Match 11.3%; Score 196.8; DB 1; Length 1933;
 Best Local Similarity 53.9%; Pred. No. 3.2e-28;
 Matches 455; Conservative 0; Mismatches 377; Indels 12; Gaps 2;

QY 183 AGAAATGCTAATTTCAATAAATCTTCCTGCCACATCTCCATCATCTTTAAAC 242
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 146 AGAAATGAGACACTCAACAAATATGTGTATCATCCCTATGCCCTATGTCTCTCT 205
 QY 243 TGGCATTTGGGCAATGATGGTATCCCTGGTCAATGGGTTACAGAGAAACTGAGAAG 302
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 206 GAGCCTGCTGGGAAACTCCCTGTGATGCTGATCTTATACAGACAGAGTGGCGCTC 265
 QY 303 CATGACGCAAGTACAGAGTGCACCTGTCATGTCAGTGGCCACCTCTTTGTCATACGCT 362
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 266 GGTCACTATGTCTACCTGCTGAACTGGCTGGCCGACACTCTTTGGCCCTACCTT 325
 QY 363 TCCCTTTGGGCAATGATGCGGTGCAAACTGTACTTTGGGAACTTCATTCAGAGC 422
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 326 GCCATCTGGGGCGGCTCCAGATGATGCTGGATTTTGGCAATTCCTGTGAAAGT 385
 QY 423 AGTCATATCATCTACACAGTCACTCTACAGAGTGTCTCTCATCTGGCCCTTATCAG 482
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 386 GGTCACTCTCTGAGAGGATCACTTCTACAGTGGCATCCGCTGTGGCTGATCAG 445
 QY 483 TGTGACCGGCTACCTGGGCACTGCTCCAGCCCAACAGTACAGAGCCAGAGAGCTTT 542
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 446 TGTGACCGGCTACCTGGGCACTGCTCCAGCCCAACAGTACAGAGCCAGAGAGCTTT 505
 QY 543 GCGTGAAGAGTGTCTATGTTGGCTGTGATCCCTCCCTCCTGACATATTCGCGA 602
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 506 G---GTCAAGTTGTTGTTGCTGGCTGGGAGTGTCTATGATCTGTCCCTGCTT 562
 QY 603 CTTCATCTTTGCCAAGTCACTGAGGAGAGTACAGATATATCTGT-----GACCG 653
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 563 CTTCCTTTCCGCGGCTTACATCAACCAATCCAGTCCAGTTTCTATGAGAGTCT 622
 QY 654 CTTCACCCCAATGACTGTGGGTGTGTGTTCCAGTTTACAGCATCATGTTGGCT 713
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 623 GGGAAATACACAGAAATGCGGATGTGTGGATCTGCTCCTACACCTTTGGGCTT 682
 QY 714 TATCCTGCTGATATTCATCTCTCTGATTCATATTCATCTCAAGCTTCACA 773
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 683 CATGTGCGGCTGTTGTCATGCTGTCTGCTATGATTCACCTGCGCTAATGCTTTAA 742
 QY 774 CTCCAGGGCCACAGAGGCGCAAGCCCTCAAGACACAGTCACTCATCTGCTGCTT 833
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 743 GGGCCACATGAGGAGAGACCGGATGAGGCTCATCTTTGCTGTGCTCATCTT 802
 QY 834 CTTCGCTGTTGGCTGCTTACTATGATGGATCAGATCAGCTCTTCATCTCTGGA 893
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 803 CCTGCTTTGCTGGCTGCTCAACCTGCTGCTGAGACACCTCATGAGAGCCCA 862
 QY 894 AATCATCAAGCAAGGCTGTGATGAGACACTGTGACAAAGTATTCATCTCAACGA 953
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 863 GGTATTCAGAGAGACTGTGAGACCGCAACACATCGCGGCGGCTGTGATGCCATGA 922
 QY 954 GGCCTACGCTTTCTTCACACTGTGTGTGTAACCCATCTCTATGCTTCTTGGAGCCA 1013

Db 923 GATTCGTGGATTTCCATACCTGCTCAACCCCATCATCTACCGCCATTCAGGCCAAA 982
 QY 1014 ATTT 1017
 ||||
 Db 983 TTTT 986

RESULT 14
 ID 080520 standard; cDNA; 1933 BP.
 AC 080520;
 DT 18-JUL-1995 (first entry)
 DE Interleukin-8 receptor cDNA insert.
 KW Interleukin-8 receptor; IL-8 receptor; PF4R;
 KW platelet factor superfamily receptor; neutrophil; chemotactic;
 KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
 KW fibrosis; colitis; bronchitis; meningitis; therapeutic; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 51..1103
 FT /tag- a
 PN W09428931-A.
 PD 22-DEC-1994.
 PF 07-JUN-1994; U06380.
 PR 11-JUN-1993; US-076093.
 PA (GETH) GENENTECH INC.
 PI Chuntarapai A, Hebert C, Kim KJ, Lee J;
 DR WPI: 95-036114/05.
 DR P-PSDB: R68811.
 PT Treatment of inflammatory disorders - by administering an
 PT antibody capable of binding a platelet factor 4 superfamily
 PT receptor polypeptide
 PS Disclosure, Page 51-54; 83pp; English.
 CC A cDNA library constructed from human neutrophil mRNA in pRK5B was
 CC transfected into COS-7 cells, and the cells were screened with 125I-
 CC IL-8. The DNA sequence of isolated cDNA clone pRK5B.118r1.1,
 CC encoding human IL-8 receptor, is given in 080520 and the predicted
 CC amino acid sequence in R68811. The receptor is used to raise
 CC antibodies that neutralize the activity of PF4R, e.g. IL-8 receptor.
 SO Sequence 1933 BP; 422 A; 540 C; 485 G; 486 T;

Query Match 11.3%; Score 196.8; DB 1; Length 1933;
 Best Local Similarity 53.9%; Pred. No. 3.2e-28;
 Matches 455; Conservative 0; Mismatches 377; Indels 12; Gaps 2;

QY 183 AGAAATGCTAATTTCAATAAATCTTCCTGCCACATCTCCATCATCTTTAAAC 242
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 146 AGAAATGAGACACTCAACAAATATGTGTATCATCCCTATGCCCTATGTCTCTCT 205
 QY 243 TGGCATTTGGGCAATGATGGTATCCCTGGTCAATGGGTTACAGAGAACTGAGAAG 302
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 206 GAGCCTGCTGGGAAACTCCCTGTGATGCTGATCTTATACAGACAGAGTGGCGCTC 265
 QY 303 CATGACGCAAGTACAGAGTGCACCTGTCATGTCAGTGGCCACCTCTTTGTCATACGCT 362
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 266 GGTCACTATGTCTACCTGCTGAACTGGCTGGCCGACACTCTTTGGCCCTACCTT 325
 QY 363 TCCCTTTGGGCAATGATGCGGTGCAAACTGTACTTTGGGAACTTCATTCAGAGC 422
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 326 GCCATCTGGGGCGGCTCCAGATGATGCTGGATTTTGGCAATTCCTGTGAAAGT 385
 QY 423 AGTCATATCATCTACACAGTCACTCTACAGAGTGTCTCTCATCTGGCCCTTATCAG 482
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 386 GGTCACTCTCTGAGAGGATCACTTCTACAGTGGCATCCGCTGTGGCTGATCAG 445
 QY 483 TGTGACCGGCTACCTGGGCACTGCTCCAGCCCAACAGTACAGAGCCAGAGAGCTTT 542
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 446 TGTGACCGGCTACCTGGGCACTGCTCCAGCCCAACAGTACAGAGCCAGAGAGCTTT 505
 QY 543 GCGTGAAGAGTGTCTATGTTGGCTGTGATCCCTCCCTCCTGACATATTCGCGA 602
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 14, 1999, 09:52:23 : Search time 465.14 Seconds
(without alignments)
11876.419 Million cell updates/sec

Title: US-09-104-063-3

Sequence: 1 GAATTCACAGTGTCTGCGCG.....CCGCCACACACTGGAATTC 1737

Scoring table: IDENTITY_NUC

Searched: 679419 seqs, 1590154680 residues

Database :

GenEmbl.*
1: gb_bal.*
2: gb_ba2.*
3: gb_om.*
4: gb_ov.*
5: gb_pat.*
6: gb_ph.*
7: gb_pl.*
8: gb_pl2.*
9: gb_pr1.*
10: gb_pr2.*
11: gb_pr3.*
12: gb_ro.*
13: gb_st.*
14: gb_sts.*
15: gb_sy.*
16: gb_un.*
17: gb_vi.*
18: em_fun.*
19: em_hlg.*
20: em_hum1.*
21: em_hum2.*
22: em_in.*
23: em_om.*
24: em_or.*
25: em_ov.*
26: em_pat.*
27: em_ph.*
28: em_pl.*
29: em_ro.*
30: em_sts.*
31: em_sy.*
32: em_un.*
33: em_vi.*
34: gb_hlg.*
35: gb_hlg2.*
36: gb_in1.*
37: gb_in2.*
38: em_ba1.*
39: em_ba2.*
40: em_hum3.*
41: em_hum4.*
42: gb_pr4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1737	100.0	1737	5	AR015970 Sequence

2	1737	100.0	1737	5	113753	113753 Sequence 4
3	1737	100.0	1737	5	124455	124455 Sequence 3
4	1653.4	95.2	1664	9	HUMHM89	D10924 Human mRNA
5	1653.4	95.2	1664	14	G28514	G28514 human STS S
6	1642	94.5	1645	10	HSNPR1A	X71635 H.sapiens m
7	1625.2	93.6	1670	9	HUMGPCR	L06797 Human (clon
8	1564	90.0	5161	11	AF005058	AF005058 Homo sapi
9	1562.4	89.9	8747	9	HS4224869	AJ224869 Homo sapi
10	1562.4	89.9	8747	11	AF052572	AF052572 Homo sapi
11	1556.4	89.6	1637	9	HUMGSTR	M99293 Homo sapien
12	1536	88.4	3733	10	HSCXCR4	Y14739 Homo sapien
13	1266.6	72.9	1689	9	FC49816	AJ09816 Felis cat
14	1213	69.8	1225	9	HUMNTRCA	L01639 Human (clon
15	1084.6	62.4	1126	11	AF019378	AF019378 Cercopith
16	1083.8	62.4	1087	11	PT089798	U89798 Pan troglod
17	1059	61.0	1059	11	AF025375	AF025375 Homo sapi
18	1048.6	60.4	1087	11	AF001928	AF001928 Macaca mu
19	1042.8	60.0	1078	9	D86579	D86579 Macaca fasc
20	1027	59.1	1059	11	AF031089	AF031089 Papio ham
21	1024.8	59.0	1068	9	AB015943	AB015943 Chloroceb
22	1020.6	58.8	1059	10	MMU93311	U93311 Macaca mula
23	1020.6	58.8	1059	11	MMU73740	U73740 Macaca mula
24	1007.8	58.0	1059	11	AF051906	AF051906 Cercopetu
25	998.4	57.5	1280	3	BOVNYR	M86739 Cow neurope
26	974.4	56.1	1877	12	D87747	D87747 Mus musculu
27	950.6	54.7	1170	3	FCU63538	U63538 Felis catus
28	936.8	53.9	1575	12	MBLESTRPT	X99582 M.musculus
29	935.8	53.9	1809	12	AB000803	AB000803 Mouse mRN
30	923.6	53.2	3770	12	MLESTRGN	X99581 M.musculus
31	914.2	52.6	1140	3	FCU92795	U92795 Felis catus
32	846.4	48.7	1223	12	MMU59760	U59760 Mus musculu
33	845.8	48.7	1422	12	MMUCR13	Z80113 Mus musculu
34	844.4	48.6	1180	12	MMUCR12	Z80112 Mus musculu
35	804.6	46.3	3366	12	MMU65580	U65580 Mus musculu
36	804	46.3	1050	12	RNU90610	U90610 Rattus norv
37	762.2	43.9	1362	12	RNU54791	U54791 Rattus norv
38	545	31.4	2090	4	XLA17894	Y17894 Xenopus lae
39	542.8	31.2	2264	4	XLA17895	Y17895 Xenopus lae
40	462.8	26.6	378	3	OAUC8942	U38942 Ovis aries
41	433.6	25.0	1681	4	OMCXCRC	AJ001039 Oncomyrnc
42	398	22.9	1632	4	AB012310	AB012310 Cyprinus
43	377.4	21.7	528	12	MMUCR11	Z80111 Mus musculu
44	206.8	11.9	1068	3	RAB1L8C	M74240 Oryctolagus
45	206.8	11.9	1232	3	RAB1L8BRC	M82873 Oryctolagus

ALIGNMENTS

RESULT 1	AR015970	1737 bp	DNA	PAT	04-DEC-1998
LOCUS	AR015970	Sequence 3 from patent US 5776457.			
DEFINITION	AR015970				
ACCESSION	93972247				
NID	93972247				
VERSION	AR015970.1	GI:3972247			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1737)				
AUTHORS	Iee,J. and Wood,W.I.				
TITLE	Antibodies to human PR4A receptor and compositions thereof				
JOURNAL	Patent: US 5776457-A 3 07-JUL-1998;				
FEATURES	Location/Qualifiers				
source	1..1737				
BASE COUNT	454 a 411 c 373 g 499 t				
ORIGIN	/organism="unknown"				

Query Match 100.0%; Score 1737; DB 5; Length 1737;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1737: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 GAATTCACAGTGTGCTGGCGCGCGGCAAGTACAGCCGAGGCGCTGAGTGTCCAGTA 60
DB 1 GAATTCACAGTGTGCTGGCGCGCGGCAAGTACAGCCGAGGCGCTGAGTGTCCAGTA 60
OY 61 GCCACCGCATCTGGAGAACAGCGGTACCATGAGAGGGATCATATATACACTTCAGAT 120
DB 61 GCCACCGCATCTGGAGAACAGCGGTACCATGAGAGGGATCATATATACACTTCAGAT 120
OY 121 AACTACACCGAGGAATGGGCTCAGGGAGTATGACTCCATGAGGAACCCCTGTTCGGT 180
DB 121 AACTACACCGAGGAATGGGCTCAGGGAGTATGACTCCATGAGGAACCCCTGTTCGGT 180
OY 181 GAAGAAATGCTAATTTCAATAAAATCTTCCTGCGCCACCATCATCATCTCTCTTA 240
DB 181 GAAGAAATGCTAATTTCAATAAAATCTTCCTGCGCCACCATCATCATCTCTCTTA 240
OY 241 ACTGGCATTTGGGCAATGGATGTGCATCTGTGTCATGGGTTACCAAGAAACTGAGA 300
DB 241 ACTGGCATTTGGGCAATGGATGTGCATCTGTGTCATGGGTTACCAAGAAACTGAGA 300
OY 301 AGCATACGAGCAAGTACAGAGCTGCACCTGTGTCATGGGTTACCAAGAAACTGAGA 360
DB 301 AGCATACGAGCAAGTACAGAGCTGCACCTGTGTCATGGGTTACCAAGAAACTGAGA 360
OY 361 CTTCCTCTGGGCAATGGATGTGCATCTGTGTCATGGGTTACCAAGAAACTGAGA 420
DB 361 CTTCCTCTGGGCAATGGATGTGCATCTGTGTCATGGGTTACCAAGAAACTGAGA 420
OY 421 GGAGTCATGTGTCATACAGAGTCAACCTCTACAGAGTGTCTCTCTCTCTCTCTATC 480
DB 421 GGAGTCATGTGTCATACAGAGTCAACCTCTACAGAGTGTCTCTCTCTCTCTCTATC 480
OY 481 AGTCTGAGAGCGTACTGCTGCGCATCTGTCACAGCGCCACCAAGTACAGAGCGGCA 540
DB 481 AGTCTGAGAGCGTACTGCTGCGCATCTGTCACAGCGCCACCAAGTACAGAGCGGCA 540
OY 541 TTGGCTGAAGAGTGTGTCATGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 600
DB 541 TTGGCTGAAGAGTGTGTCATGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 600
OY 601 GACTTCATCTTTGCCAAGCTCAGTACAGAGGAGATGACAGATATATCTGTACCGCTCT 660
DB 601 GACTTCATCTTTGCCAAGCTCAGTACAGAGGAGATGACAGATATATCTGTACCGCTCT 660
OY 661 CCCAATGACTTGTGGGTGTGTGTCAGTTTCACCAATCATATGTTGGCTTATCTCTG 720
DB 661 CCCAATGACTTGTGGGTGTGTGTCAGTTTCACCAATCATATGTTGGCTTATCTCTG 720
OY 721 CCTGATATGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 CCTGATATGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
OY 781 GGGCACCAGAGGAGGAGGCGCTCAAGACACAGTATCTCTCTCTCTCTCTCTCTG 840
DB 781 GGGCACCAGAGGAGGAGGCGCTCAAGACACAGTATCTCTCTCTCTCTCTCTCTG 840
OY 841 TGTGCTGCTCTTACTACATTTGGGATGAGTATGACTCTCTCTCTCTCTCTCTCTG 900
DB 841 TGTGCTGCTCTTACTACATTTGGGATGAGTATGACTCTCTCTCTCTCTCTCTCTG 900
OY 901 AAGCAAGGAGTGTGATTTAGAAACATGTGCAAGTGTGATTTCCATCCGAGGCGCTA 960
DB 901 AAGCAAGGAGTGTGATTTAGAAACATGTGCAAGTGTGATTTCCATCCGAGGCGCTA 960
OY 961 GCTTTCTTCTACATGTGTGTAACCCCATCTCTATCTCTCTCTCTCTCTCTCTCTA 1020
DB 961 GCTTTCTTCTACATGTGTGTAACCCCATCTCTATCTCTCTCTCTCTCTCTCTCTA 1020
OY 1021 ACCTCTGCGCAGCAGCACTACCTCTGTGAGCAGAGGGTCCAGCTCAAGATCTCTCTC 1080
DB 1021 ACCTCTGCGCAGCAGCACTACCTCTGTGAGCAGAGGGTCCAGCTCAAGATCTCTCTC 1080

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OY 1081 AAAGAAAGCGAGTGTGACATTCATCTGTTCCACTGAGTGTGAGTCTTCAAGTTTTCAC 1140
DB 1081 AAAGAAAGCGAGTGTGACATTCATCTGTTCCACTGAGTGTGAGTCTTCAAGTTTTCAC 1140
OY 1141 TCCAGCTAACACAGATGTAAAGACTTTTTTTTATACGATAAATTAACTTTTTTTAACTT 1200
DB 1141 TCCAGCTAACACAGATGTAAAGACTTTTTTTTATACGATAAATTAACTTTTTTTAACTT 1200
OY 1201 ACACATTTTTCAGATATATAAGACTGACCAATATGTACAGTTTTTATGCTGTGGAT 1260
DB 1201 ACACATTTTTCAGATATATAAGACTGACCAATATGTACAGTTTTTATGCTGTGGAT 1260
OY 1261 TTTGCTGTGTTCTCTTATAGTTTGTGAGATTTTGAAGTTTAAATGCTTATATATTTT 1320
DB 1261 TTTGCTGTGTTCTCTTATAGTTTGTGAGATTTTGAAGTTTAAATGCTTATATTTT 1320
OY 1321 TTTGTTTCATATTTGATGTGTGTCTAGGAGACCTGTGGCAAGTCTTATGCTGTAT 1380
DB 1321 TTTGTTTCATATTTGATGTGTGTCTAGGAGACCTGTGGCAAGTCTTATGCTGTAT 1380
OY 1381 GTCTGCTGTAGAGTGTAGAAAAGGAACTGACATTCAGAGCGTGTAGTAATCACG 1440
DB 1381 GTCTGCTGTAGAGTGTAGAAAAGGAACTGACATTCAGAGCGTGTAGTAATCACG 1440
OY 1441 TTAAGCTGAAGTATGATCCCAAGCTTTATGATGATATCTCCATTCCTCCGAGAAC 1500
DB 1441 TTAAGCTGAAGTATGATCCCAAGCTTTATGATGATATCTCCATTCCTCCGAGAAC 1500
OY 1501 GTTTTCTGTCTTAAAGCTGATTTTGTGTAGAGAGTGGCACTTAAACAAAGCCC 1560
DB 1501 GTTTTCTGTCTTAAAGCTGATTTTGTGTAGAGAGTGGCACTTAAACAAAGCCC 1560
OY 1561 AAAGTGTATGAATGCTGTTTTCAGTTTTCAGAGTGGTGTGATTTACAGACCTTAC 1620
DB 1561 AAAGTGTATGAATGCTGTTTTCAGTTTTCAGAGTGGTGTGATTTACAGACCTTAC 1620
OY 1621 AGTGTACAGTCTTGTATTAAGTGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1680
DB 1621 AGTGTACAGTCTTGTATTAAGTGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1680
OY 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1737
DB 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1737

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RESULT 2

LOCUS	113753	1737 bp	DNA	PAT	18-SEP-1995
DEFINITION	Sequence	4 from patent	US 5440021.		
ACCESSION	113753				
KEYWORDS	9996819				
VERSION	113753.1	GI:996819			
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1737)				
AUTHORS	Chuncharapal, A., Hebert, C., Kim, K.J. and Lee, J.				
TITLE	Antibodies to human IL-8 type B receptor				
JOURNAL	Patent: US 5440021-A 4 08-Aug-1995;				
FEATURES	Location/Qualifiers				
source	1..1737				
BASE COUNT	454 a 411 c 373 g 499 t				
ORIGIN					

Query Match 100.0%; Score 1737; DB 5; Length 1737;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1737: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GAATTCACAGTGTGCTGGCGCGCGGCAAGTACAGCCGAGGCGCTGAGTGTCCAGTA 60

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Db 1 GAATTCAGTGTGCTGGCGCGCGCCGCAAGTACCGCCGAGGCGCTGATGCTCCAGTA 60
QY 61 GCCACCCGATCTGGAGAACGCGGTTACCATGGAGGGATCAGTATATACACTTCAGAT 120
Db 61 GCCACCCGATCTGGAGAACGCGGTTACCATGGAGGGATCAGTATATACACTTCAGAT 120
QY 121 AACACACCCGAGAAATGGGCTCAGGGGACATATCTCATGAAGAAACCTGTTCCGT 180
Db 121 AACACACCCGAGAAATGGGCTCAGGGGACATATCTCATGAAGAAACCTGTTCCGT 180
QY 181 GAAGAAATGCTATTTCAATAAATCTCCGCGCAACATCTACTCATCATCTTCTTA 240
Db 181 GAAGAAATGCTATTTCAATAAATCTCCGCGCAACATCTACTCATCATCTTCTTA 240
QY 241 ACTGGCATTTGGGCGCAATGGATGGTCACTCTGTCATGGGTTACGAGAAAGAACTGAGA 300
Db 241 ACTGGCATTTGGGCGCAATGGATGGTCACTCTGTCATGGGTTACGAGAAAGAACTGAGA 300
QY 301 AGCATGACGACAGTACAGGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 360
Db 301 AGCATGACGACAGTACAGGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 360
QY 361 CTTCCTCTTGGGCGATTTGATGCGCGTGGCAAACTGATTTGGGAACTTCTTATGCAAG 420
Db 361 CTTCCTCTTGGGCGATTTGATGCGCGTGGCAAACTGATTTGGGAACTTCTTATGCAAG 420
QY 421 GCAGTCCATGTCATCTACACAGTACCTCTACAGAGTGTCTCATCTCTGCGCTTATC 480
Db 421 GCAGTCCATGTCATCTACACAGTACCTCTACAGAGTGTCTCATCTCTGCGCTTATC 480
QY 481 AGTGTGACCGCTACCTGCGCATGTCCAGGCGCAACAGTCCAGAGGCGCAAGAACTG 540
Db 481 AGTGTGACCGCTACCTGCGCATGTCCAGGCGCAACAGTCCAGAGGCGCAAGAACTG 540
QY 541 TTGGCTGAAAGAGTGTCTATGTTGGCGTGTGATCCCTGCGCTGCTGATCTATCC 600
Db 541 TTGGCTGAAAGAGTGTCTATGTTGGCGTGTGATCCCTGCGCTGCTGATCTATCC 600
QY 601 GACTTCATCTTTGCCAACGTCAGTGAAGGAGATGACAGATATATCTGTGACCGCTTAC 660
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Db 661 CCCAATGACTTGTGGGCGTGTGTTCTCAGTTTACGACATCATGTTGGCTTATCTG 720
QY 721 CCTGATTTGTCATCTCTGCTGCTATGATATCATCTCCAGCTGTGACACTCCAG 780
Db 721 CCTGATTTGTCATCTCTGCTGCTATGATATCATCTCCAGCTGTGACACTCCAG 780
QY 781 GGGCACCAGAGGCGCAGGCGCTCAAGACACAGTCACTCTCATCTGCGCTTCTTGGC 840
Db 781 GGGCACCAGAGGCGCAGGCGCTCAAGACACAGTCACTCTCATCTGCGCTTCTTGGC 840
QY 841 TGTGTCGTCCTTACTACATTTGGGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 900
Db 841 TGTGTCGTCCTTACTACATTTGGGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 900
QY 901 AAGCAAGGCTGTAGTTGAGAACACTGTGCACAAAGTGTGATTTCCATCCAGGAGCCCTA 960
Db 901 AAGCAAGGCTGTAGTTGAGAACACTGTGCACAAAGTGTGATTTCCATCCAGGAGCCCTA 960
QY 961 GCTTCTTCACATGTTGTGAAACCCCATCTCATGCTTCTTCTGAGGCAAAATTTAAA 1020
Db 961 GCTTCTTCACATGTTGTGAAACCCCATCTCATGCTTCTTCTGAGGCAAAATTTAAA 1020
QY 1021 ACCTTCGCCAGCAGCAGTACCTCTGTGAGCAGAGAGGTCGACGCTCAAGATCTCTCC 1080
Db 1021 ACCTTCGCCAGCAGCAGTACCTCTGTGAGCAGAGAGGTCGACGCTCAAGATCTCTCC 1080
QY 1081 AAAGGAAGGAGGTGACATTCATCTGTTCCAGTGTGAGTTCAGATTTTCCAC 1140
Db 1081 AAAGGAAGGAGGTGACATTCATCTGTTCCAGTGTGAGTTCAGATTTTCCAC 1140

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Db 1081 AAAGGAAGGAGGTGACATTCATCTGTTCCAGTGTGAGTTCAGATTTTCCAC 1140
QY 1141 TCCAGCTAACACAGATGATAAAGACTTTTATATAGATTAATTAATTTTAAAGTT 1200
Db 1141 TCCAGCTAACACAGATGATAAAGACTTTTATATAGATTAATTAATTTTAAAGTT 1200
QY 1201 ACACATTTTTCAGATATATTAAGAGTACCAATATGTACAGTATTTATTCCTGTTGGAT 1260
Db 1201 ACACATTTTTCAGATATATTAAGAGTACCAATATGTACAGTATTTATTCCTGTTGGAT 1260
QY 1261 TTTTGTCTGAGTTCTTTTATTTTGTGAGGTTTATTAATTAATTAATTTT 1320
Db 1261 TTTTGTCTGAGTTCTTTTATTTTGTGAGGTTTATTAATTAATTAATTTT 1320
QY 1321 TTTTGTCTGAGTTCTTTTATTTTGTGAGGTTTATTAATTAATTAATTTT 1380
Db 1321 TTTTGTCTGAGTTCTTTTATTTTGTGAGGTTTATTAATTAATTAATTTT 1380
QY 1381 GTCTCGTGTGAGTACCTTAAGAAAGGAACTGAACATTCAGAGCGTGTAGTATCAG 1440
Db 1381 GTCTCGTGTGAGTACCTTAAGAAAGGAACTGAACATTCAGAGCGTGTAGTATCAG 1440
QY 1441 TAAAGCTAGAAATGATCCCGAGCTGTTATGATATATCTCATCTCCGCTGAGAC 1500
Db 1441 TAAAGCTAGAAATGATCCCGAGCTGTTATGATATATCTCATCTCCGCTGAGAC 1500
QY 1501 GTTTTCTGTTCTTTAAGAGCTATTTTGTGAGAGATGGCACTTATTAACCAAGCCC 1560
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QY 1561 AAGTGTATAGAAATGCTGTTTTCAGTTTTCAGTGTGAGAGTGGTGTGATTCAGACCTAC 1620
Db 1561 AAGTGTATAGAAATGCTGTTTTCAGTTTTCAGTGTGAGAGTGGTGTGATTCAGACCTAC 1620
QY 1621 AGTGTACGCTCTGTTAATTAAGTTTAAATGATATTAATTAATTAATTAATTAATTAAT 1680
Db 1621 AGTGTACGCTCTGTTAATTAAGTTTAAATGATATTAATTAATTAATTAATTAATTAAT 1680
QY 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCCAGCAGTGTGAATTC 1737
Db 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCCAGCAGTGTGAATTC 1737

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RESULT 3
LOCUS 124455 1737 bp DNA PAT 14-AUG-1996
DEFINITION Sequence 3 from patent US 5543503.
ACCESSION 124455
NID 91604325
VERSION 124455.1 GI:1604325
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1737)
AUTHORS Chundharapal, A., Lee, J., Hebert, C. and Kim, K. Jin.
TITLE Antibodies to human IL-8 type A receptor
JOURNAL Patent: US 5543503-A 3 06-AUG-1996.
FEATURES
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BASE COUNT 454 a 411 c 373 g 499 t
ORIGIN

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Query Match 100.0%; Score 1737; DB 5; Length 1737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Human mRNA for HM89.
ACCESSION D10924
VERSION 9219868
KEYWORDS GTP-binding protein; plasma membrane protein; protein coupled.
SOURCE Homo sapiens monocyte, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1664)
AUTHORS Nomura, H., Nielsen, B.W. and Matsushima, K.
TITLE Molecular cloning of cDNAs encoding a LD78 receptor and putative
leukocyte chemotactic peptide receptors
JOURNAL Int. Immunol. 5 (10), 1239-1249 (1993)
COMMENT
MEDLINE 94092629
SUBMITTED (13-Apr-1992) to DBJ by:
HIDEKI NOMURA
DEPT. OF PHARMACOL.
CANCER RES. INST., KANAZAWA UNIV.
13-1 TAKARACHU
KANAZAWA, ISHIKAWA 920
JAPAN
PHONE: 0762-62-8151 x5875
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SOURCE human.
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Buthera: Primates: Catarrhini: Homidae: Homo.
REFERENCE 1 (bases 1 to 1664)
AUTHORS Myers, R.M.
JOURNAL Unpublished (1996)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myerseshgc.stanford.edu
Primer A: TTGTACAGTCTTTATGCTGTGG
Primer B: CGTATTTACTACACGCTCTGG
STS size: 207
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/uL
Total Vol: 10 uL
Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
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DEFINITION	H.sapiens mRNA for neuropeptide Y-like receptor.		
ACCESSION	X71635		
NID	9297099		
VERSION	X71635.1	GI:297099	
KEYWORDS	Chemotaxis; G-protein coupled receptor; neuropeptide Y.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
AUTHORS	Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 1645)		
JOURNAL	Moser, B.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (26-APR-1993) B. Moser, University of Bern, PO Box 99,		
TITLE	Bern, SWITZERLAND		
JOURNAL	2 (bases 1 to 1645)		
REFERENCE	Loetscher, M., Geisler, T., O'Reilly, T., Zahlen, R., Baggiolini, M. and		
AUTHORS	Moser, B.		
TITLE	Cloning of a human seven-transmembrane domain receptor, LESTR, that		
JOURNAL	is highly expressed in leukocytes		
MEDLINE	J. Biol. Chem. 269 (1), 232-237 (1994)		
FEATURES	94103215		
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QY 445	AACTCTACAGCAAGTGTCTCATCTGTGGCTTCATCACTGAGCCGCTACCTGGCCATC						
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NID 92735718
VERSION AF005058.1 GI:2735718
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

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REFERENCE
AUTHORS
Wegner,S.A., Ehrenberg,P.K., Chang,G., Dayhoff,D.E. and
Michael,N.L.
TITLE
Genomic organization and characterization of the promoter for the
HIV-1 entry co-receptor CXCR-4
JOURNAL
Unpublished
2 (bases 1 to 5161)
AUTHORS
Wegner,S.A., Ehrenberg,P.K., Chang,G., Dayhoff,D.E. and
Michael,N.L.
TITLE
Direct Submission
JOURNAL
Submitted (21-MAY-1997) Division of Retrovirology, Walter Reed Army
Institute of Research, 13 Tait Court, Suite 200, Rockville, MD
20850, USA
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 VERSION AJ224869.1 GI:3059119
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 SOURCE human.
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 REFERENCE 1 (bases 1 to 8747)
 AUTHORS Caruz, A.
 JOURNAL Direct Submission
 Submitted (06-MAR-1998) Caruz, A., Immunologie Virale, Institut
 Pasteur Paris, 28 Rue Dr. Roux Paris Cedex 15, 75724, FRANCE
 REFERENCE 2 (bases 1 to 8747)
 AUTHORS Caruz, A., Sansom, M., Alonso, J. M., Alcamí, J., Balleux, F.,
 Virelizier, J. L., Parmentier, M., and Arenzana-Seisdedos, F.
 TITLE Genomic organization and promoter characterization of human CXCR4
 JOURNAL FEBS Lett. 426 (2), 271-278 (1998)
 MEDLINE 98258970
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 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 8747)
 AUTHORS Caruz, A., Samsom, M., Alonso, J. M., Alcamí, J., Balazs, F.,
 Virelizier, J. L., Parmentier, M. and Arenzana-Seisdedos, F.
 TITLE gene
 JOURNAL FEBS Lett. 426 (2), 271-278 (1998)
 MEDLINE 98258970
 REFERENCE 2 (bases 1 to 8747)
 AUTHORS Caruz, A., Samsom, M., Virelizier, J. L., Parmentier, M. and
 Arenzana-Seisdedos, F.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAR-1998) Immunologie Virale, Institut Pasteur, 28
 Rue Dr Roux, Paris 75724, France
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QY	1486	CCATTCGGTGGAGAGCTTTTTCGTCTTAAGACGTGATTTTGGCTGTAAGATGGAC	1545
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QY	1546	TATAACCAAAAGCCCAAGTGTATAGAAATGCTGTTTTCAGTTTTCAGAGTGGTT	1605
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QY	1606	GATTTCAGACCTACTACAGTGTATAGTGTATTAAGTTGTTAATAAGTACATGTTAA	1665
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QY	1666	CTTA 1669	
Db	6428	CTTA 6431	
RESULT	11		
LOCUS	HUMSTR	1637 bp	mrna
DEFINITION	Homo sapiens seven transmembrane segment receptor mRNA, complete cds.		PRI 10-MAR-1994
ACCESSION	M99293		
VERSION	G282516		
KEYWORDS	M99293.1 GI:292516		
SOURCE	seven transmembrane segment receptor.		
ORGANISM	Homo sapiens (human).		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 1637)		
JOURNAL	Federpiel, B., Melhado, I.G., Duncan, A.M., Delaney, A., Schappert, K., Clark-Lewis, I., and Jirik, F.R.		
MEDLINE	Molecular cloning of the cDNA and chromosomal localization of the gene for a putative seven-transmembrane segment (7-TMS) receptor isolated from human spleen		
FEATURES	Genomics 16, 707-712 (1993)		
source	93315164		
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Best Local Similarity	98.7%: Pred. No. 2e-272;		
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QY	136	ATGGGCTCAGGGGACTATGATCTCATGAAAGAACCGTTCCGTCAAGAAATGCTAT	195
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QY	616	AACGTCAGTAGGCGAGATGACAGATATATCTGTACCGCTTCTACCCCATGACTTTGG	675
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QY	676	GTCGTTGTGTCACAGTTTACAGCATATGTTGGGCTTATCCTGTGCTGGTATTTGTCATC	735
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QY	736	CTGTCTGCTATTGCAATTATATCTCTCAAGCTGTCACTCCAGAGGCCACCAAGAGCG	795
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QY	796	AAGGCCCTCAAGACACAGTCATCTCATCTGATCGGCTTCTTGCGCTTTGGGTGGCTTAC	855
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QY	1036	GCACACACCTCTGTGACACAAGGGTCCAGCTCAACATCTCTCCAAAGGAAGGAGGT	1095
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 ACCESSION Y14739
 NID 93021393
 VERSION Y14739.1 GI:3021393
 KEYWORDS Chemokine receptor; CXCR4 gene.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 3733)
 AUTHORS Froidl, R., Moeppl, B. and Gierschik, P.
 TITLE Genomic organization and expression pattern of the human chemokine
 receptor CXCR4
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3733)
 AUTHORS Froidl, R.
 TITLE Direct Submission
 JOURNAL Submitted (03-SEP-1997) R. Froidl, Department of Pharmacology and
 Toxicology, Albert-Einstein-Allee 11, University of Ulm, 89081 Ulm,
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 REMARK revised by submitter 31-MAR-1998
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RESULT 13
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LOCUS      Fc9816
DEFINITION Fc9816 mRNA for CXCR4 chemokine receptor.
ACCESSION AJ009816
NID        94200300
VERSION    AJ009816.1 GI:4200300
KEYWORDS   cell surface receptor; chemokine receptor; CXCR4 gene.
SOURCE     cat.
ORGANISM   Felis catus
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REFERENCE 1 (bases 1 to 1689)
AUTHORS   Kovacs,E.M., Baxter,G.D. and Robinson,M.F.
TITLE      Feline peripheral blood mononuclear cells express message for both
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JOURNAL    Arch. Virol. 144, 273-285 (1999)
AUTHORS     Kovacs,E.M.
REFERENCE   2 (bases 1 to 1689)
TITLE      Direct Submission
AUTHORS     Submitted (27-JUL-1998) Kovacs E.M., Department of Medicine, The
           Princess Alexandra Hospital, First Floor, Lions Research Unit,
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 HUMANRECA 1225 bp mRNA PRI 09-MAR-1994
 LOCUS HUMNYRECA 1225 bp mRNA PRI 09-MAR-1994
 DEFINITION Homo sapiens (clone HSX3R) neurotrophin Y receptor (NPYR) mRNA, complete cds.
 ACCESSION L01639
 NID 9189313
 VERSION L01639.1 GI:189313
 KEYWORDS homologous region; neurotrophin Y receptor.
 SOURCE Homo sapiens (library: Stratagene lambda-ZAPII) female 17-18 week gestation brain cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1225)
 Jazin, E.E., Yoo, H., Blomqvist, A.G., Yee, F., Weng, G., Walker, M.W., Salton, J., Larhammar, D. and Wahlstedt, C.
 A proposed bovine neurotrophin Y (NPY) receptor cDNA clone, or its human homologue, confers neither NPY binding sites nor NPY responsiveness on transfected cells
 Regul. Pept. 47 (3), 247-258 (1993)
 JOURNAL MEDLINE
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RESULT 15
AF019378
LOCUS AF019378 1126 bp mRNA PRI 02-JAN-1999
DEFINITION Cercopithecus aethiops G-protein coupled receptor (CXCR4) mRNA,
complete cds.
ACCESSION AF019378
NID 94102991
VERSION AF019378.1 GI:4102991
KEYWORDS
SOURCE African green monkey.
ORGANISM Chlorocebus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;
Chlorocebus.
REFERENCE 1 (bases 1 to 1126)
AUTHORS Holtkamp,N., Baier,M. and Werner,A.
TITLE CXCR4 from African green monkey
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1126)
AUTHORS Holtkamp,N., Baier,M. and Werner,A.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-1997) 6/3, Paul-Ehrlich-Institut,
Paul-Ehrlich-Str.51-59, Langen 63225, Germany
location/Qualifiers
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BASE COUNT 254 a 318 c 260 g 294 t
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Query Match 62.4%; Score 1084.6; DB 11; Length 1126;
Best Local Similarity 97.9%; Pred. No. 4,1e-187;
Matches 1099; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Job time: 915 sec

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RESULT 2
US-08-076-093A-3
Sequence 3, Application US/08076093A
Patent No. 5543503
GENERAL INFORMATION:
APPLICANT: Chunharapal, Anan
APPLICANT: ~~Lee, James~~
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFA4 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530
TELEX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-076-093A-3

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Db	1321	TTTGTTCATATGTATGTGTGTGTAGCAGAGACCTGTGGCCAGTTCTAGTGTGTAT	138
Qy	1381	GTCCTGTGTGATGACGTGTAGAAAAAGGAACTGAACATTCGAGCGGTGTAGTGAATCAG	144
Db	1381	GTCCTGTGTGATGACGTGTAGAAAAAGGAACTGAACATTCGAGCGGTGTAGTGAATCAG	144
Qy	1441	TAAAGCTGAATATGATCCCAAGCGTTTATGACATAGATATCTCCCATTTCCCGTGGAC	150
Db	1441	TAAAGCTGAATATGATCCCAAGCGTTTATGACATAGATATCTCCCATTTCCCGTGGAC	150
Qy	1501	GTTTTCTCTGTTCTTAAAGCGTATTTTGTGTGTAGAAAGATGGCACTTAATACCAAGCCC	156
Db	1501	GTTTTCTCTGTTCTTAAAGCGTATTTTGTGTGTAGAAAGATGGCACTTAATACCAAGCCC	156
Qy	1561	AAAGTGTATGAATACGTGTTTTCAGTTTTCAGAGATGGGTGTATTTACACACTAC	162
Db	1561	AAAGTGTATGAATACGTGTTTTCAGTTTTCAGAGATGGGTGTATTTACACACTAC	162
Qy	1621	AGTGTACAGTGTGTATTAAGTTGTATAAAGTACATTTAACTTTAAAAAATTTAA	168
Db	1621	AGTGTACAGTGTGTATTAAGTTGTATAAAGTACATTTAACTTTAAAAAATTTAA	168
Qy	1681	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACGACACTGGAATTC	1737
Db	1681	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACGACACTGGAATTC	1737
RESULT 3			
US-08-701-265-3			
; Sequence 3, Application US/08701265			
; Patent No. 5776457			
; GENERAL INFORMATION:			
; APPLICANT: Chunharapai, Anan			
; APPLICANT: <u>Lee, James</u>			
; APPLICANT: <u>Hebert, Caroline</u>			
; APPLICANT: Jin Kim, K.			
; TITLE OF INVENTION: Antibodies to Human PFAA Receptors			
; NUMBER OF SEQUENCES: 6			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Genentech, Inc.			

STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Minipath (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/701,265
 FILING DATE: 22-AUG-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/076093
 FILING DATE: 11-Jun-1993
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/677211
 FILING DATE: 29-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: 706P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1737 nucleotides
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-08-701-265-3

Query Match 100.0%; Score 1737; DB 3; Length 1737;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAATTCAGTGTGCTGGCGGCGGCGCAAGTGAAGCCGAGGCGCTGAGTGTCCAGTA 60
 1 GAATTCAGTGTGCTGGCGGCGGCGGCGCAAGTGAAGCCGAGGCGCTGAGTGTCCAGTA 60
 61 GCCACCGCATCTGGAGAACCGGCTTACCATGAGGGGATCAGTATATACACTTCAGAT 120
 61 GCCACCGCATCTGGAGAACCGGCTTACCATGAGGGGATCAGTATATACACTTCAGAT 120
 121 AACTACCGAGGAATGGGCTCAGGGGACTATGACTCCATGAAGAACCCGTTCCGT 180
 121 AACTACCGAGGAATGGGCTCAGGGGACTATGACTCCATGAAGAACCCGTTCCGT 180
 181 GAAGAAATGCTAATTTCAATAAAATCTTCTGCCACCATCATCTCAATCTTCTTA 240
 181 GAAGAAATGCTAATTTCAATAAAATCTTCTGCCACCATCATCTCAATCTTCTTA 240
 241 ACTGCGATTGGGCAATGATGATGCTCATCTGTCATGATGATGATGATGATGATGAT 300
 241 ACTGCGATTGGGCAATGATGATGCTCATCTGTCATGATGATGATGATGATGATGAT 300
 301 AGCATGACGAGCAATATACAGGCTGACCTGTGATGAGGCGGACCTCTCTTTGTCATCAG 360
 301 AGCATGACGAGCAATATACAGGCTGACCTGTGATGAGGCGGACCTCTCTTTGTCATCAG 360
 361 CTTCCTTCTGGGAGTTATGCTGCGGCAAACTGGTACTTTGGGAACTTCTTAAGCAAG 420
 361 CTTCCTTCTGGGAGTTATGCTGCGGCAAACTGGTACTTTGGGAACTTCTTAAGCAAG 420
 421 GCAGTCATGTCTATACACAGTCAACCTCTACAGCAGTGTCTCTACCTGCGCTTCATC 480
 421 GCAGTCATGTCTATACACAGTCAACCTCTACAGCAGTGTCTCTACCTGCGCTTCATC 480

421 GCAGTCATGTCTATACACAGTCAACCTCTACAGCAGTGTCTCTACCTGCGCTTCATC 480
 481 AGCTTGAGACCGCTACCTGGCCATGCTCCACGCGCACCAAGTCAAGGCGCAAGAACTG 540
 481 AGCTTGAGACCGCTACCTGGCCATGCTCCACGCGCACCAAGTCAAGGCGCAAGAACTG 540
 541 TTGGCTGAAAAGGCTGCTATGTTGGCGTGTGATGATGATGATGATGATGATGATGAT 600
 541 TTGGCTGAAAAGGCTGCTATGTTGGCGTGTGATGATGATGATGATGATGATGATGAT 600
 601 GACTTCATCTTTGCCAAGCTGAGTGAAGGAGATGACAGATATATCTGTACCGCTTCTAC 660
 601 GACTTCATCTTTGCCAAGCTGAGTGAAGGAGATGACAGATATATCTGTACCGCTTCTAC 660
 601 GACTTCATCTTTGCCAAGCTGAGTGAAGGAGATGACAGATATATCTGTACCGCTTCTAC 660
 661 CCCAATGACTGTGGGTGGTGTGTGTCCAGTTTCAGACATCATGTTGGGCTTATCTCG 720
 661 CCCAATGACTGTGGGTGGTGTGTGTCCAGTTTCAGACATCATGTTGGGCTTATCTCG 720
 721 CCTGGATTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 721 CCTGGATTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 781 GGCACACGAAAGCGGAGGCGCTCAAGACACAGATCATCTCATCTGCTTCTTCTGCC 840
 781 GGCACACGAAAGCGGAGGCGCTCAAGACACAGATCATCTCATCTGCTTCTTCTGCC 840
 841 TCTTGGTCTGCTTACTATATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 900
 841 TCTTGGTCTGCTTACTATATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 900
 901 AAGCAAGGCTGTGATGAGAACTGTGACAGTGAAGTTCATGACAGGAGGCGCTTA 960
 901 AAGCAAGGCTGTGATGAGAACTGTGACAGTGAAGTTCATGACAGGAGGCGCTTA 960
 901 AAGCAAGGCTGTGATGAGAACTGTGACAGTGAAGTTCATGACAGGAGGCGCTTA 960
 961 GCTTCTTCTCACTGTGTGTGTAAGCCCATCTCTATGCTTCTTCTTGAAGCAATTTAA 1020
 961 GCTTCTTCTCACTGTGTGTGTAAGCCCATCTCTATGCTTCTTCTTGAAGCAATTTAA 1020
 1021 ACCCTGCGCGACGACGACACTCCTCTGTGAGCAAGGCTCCAGCTCAAGTCTCTCC 1080
 1021 ACCCTGCGCGACGACGACACTCCTCTGTGAGCAAGGCTCCAGCTCAAGTCTCTCC 1080
 1081 AAAGAAAGCGAGTGTGACATCTGCTTCCAGTGTGAGTGTGAGTGTGAGTGTGAGT 1140
 1081 AAAGAAAGCGAGTGTGACATCTGCTTCCAGTGTGAGTGTGAGTGTGAGTGTGAGT 1140
 1141 TCCAGCTAACACAGATGTAAGAACTTTTATATAGATAAATACCTTTTAAAGTT 1200
 1141 TCCAGCTAACACAGATGTAAGAACTTTTATATAGATAAATACCTTTTAAAGTT 1200
 1201 ACACATTTTTCAGATATTAAGAACTGACCAATATGTAAGTATTTATGCTTGTGAT 1260
 1201 ACACATTTTTCAGATATTAAGAACTGACCAATATGTAAGTATTTATGCTTGTGAT 1260
 1261 TTTGCTTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
 1261 TTTGCTTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
 1321 TTTGCTTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
 1321 TTTGCTTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
 1381 GTCCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 1381 GTCCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 1441 TAAAGCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 1441 TAAAGCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 1501 GTTTTCTGTTCTTAAAGCTGATTTTCTGTAGAAAGTGGCACTTAAACCAAGGCC 1560
 1501 GTTTTCTGTTCTTAAAGCTGATTTTCTGTAGAAAGTGGCACTTAAACCAAGGCC 1560
 1501 GTTTTCTGTTCTTAAAGCTGATTTTCTGTAGAAAGTGGCACTTAAACCAAGGCC 1560

QY 1561 AAGTGTATAGAAATGCTGTTTTCAGTTTCAGAGATGGTGTATTCAGACTAC 1620
DB 1561 AAGGTGTATAGAAATGCTGTTTTCAGTTTCAGAGATGGTGTATTCAGACTAC 1620
QY 1621 AGTGTACAGTCTGTATTAAGTTGTATTAAGTACATGTTAACTTAAAAA 1680
DB 1621 AGTGTACAGTCTGTATTAAGTTGTATTAAGTACATGTTAACTTAAAAA 1680
QY 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACACACTGGAATTC 1737
DB 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACACACTGGAATTC 1737

RESULT 4
US-08-284-586-3
Sequence 3, Application US/08284586
Patent No. 5840856
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-284-586-3

Query Match 100.0%; Score 1737; DB 4; Length 1737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAGTGTCTGGCGGCGGCGCAAGTACGCGGAGGCGCTGATGCTCCAGTA 60
DB 1 GAATTCAGTGTCTGGCGGCGGCGCAAGTACGCGGAGGCGCTGATGCTCCAGTA 60

QY 61 GCCACCCGATCTGTAGACACAGCGGTTACCATGAGGGGATCAGTATATACCTCAGAT 120
DB 61 GCCACCCGATCTGTAGACACAGCGGTTACCATGAGGGGATCAGTATATACCTCAGAT 120
QY 121 AACTACACGAGGAAATGGGCTCAGGGGACTATGACTCCATGAGAAACCTCTTCCT 180
DB 121 AACTACACGAGGAAATGGGCTCAGGGGACTATGACTCCATGAGAAACCTCTTCCT 180
QY 181 GAAGAAATGCTAATTTCAATAAAATCTTCGCCACCATCTACTCATCTCTCTTA 240
DB 181 GAAGAAATGCTAATTTCAATAAAATCTTCGCCACCATCTACTCATCTCTCTTA 240
QY 241 ACTGGCATTTGGGCAATGATGTTGTCATCTGTCATGAGTTACAGAAACTGAGA 300
DB 241 ACTGGCATTTGGGCAATGATGTTGTCATCTGTCATGAGTTACAGAAACTGAGA 300
QY 301 AGCATGACGACAAATGACAGCTGACACCTGTACGTGGCGGACCTCCTTGTATCAGC 360
DB 301 AGCATGACGACAAATGACAGCTGACACCTGTACGTGGCGGACCTCCTTGTATCAGC 360
QY 361 CTTCCTTTCTGGGCAATGATGCTGTCGCAAACTGTACTTTGGAACTTCTATGCAAG 420
DB 361 CTTCCTTTCTGGGCAATGATGCTGTCGCAAACTGTACTTTGGAACTTCTATGCAAG 420
QY 421 GCAGTGCATGTCTATACAGATCAACCTTACAGCAGTCTCTCATCTGCGCTTCATC 480
DB 421 GCAGTGCATGTCTATACAGATCAACCTTACAGCAGTCTCTCATCTGCGCTTCATC 480
QY 481 AGTCTGACCGCTACCTGCGCATGCTCCAGCCAGCAAGTACAGAGGCGCAAGGACTG 540
DB 481 AGTCTGACCGCTACCTGCGCATGCTCCAGCCAGCAAGTACAGAGGCGCAAGGACTG 540
QY 541 TTGGCTGAAAAAGTGCTATATGTTGGGCTGTGATCCCTGCCCCCTGCTGATATYCC 600
DB 541 TTGGCTGAAAAAGTGCTATATGTTGGGCTGTGATCCCTGCCCCCTGCTGATATYCC 600
QY 601 GACTTCATCTTCCCAACGTCATGAGGAGATGAGATATATCTGTGACCCCTCTAC 660
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DB 661 CCCAATGACTTGTGGGTTGTTGTTCCAGTTTCAGACATCATGTTGAGCTTATCTG 720
QY 721 CCTGTATTGTCTATCTGCTGCTCTATATGATATCATCTCAAGCTGTACACTCCAAG 780
DB 721 CCTGTATTGTCTATCTGCTGCTCTATATGATATCATCTCAAGCTGTACACTCCAAG 780
QY 781 GGGCACCAGAAAGGCGCAAGGCGCTCAAGACACAGTATCTCTGCTTCTTCCGC 840
DB 781 GGGCACCAGAAAGGCGCTCAAGGCGCTCAAGACACAGTATCTCTGCTTCTTCCGC 840
QY 841 TGTGGCTGCTTACTACATTTGGGATCAGATGACTCTCTCATCTCTCGAATATATC 900
DB 841 TGTGGCTGCTTACTACATTTGGGATCAGATGACTCTCTCATCTCTCGAATATATC 900
QY 901 AAGCAAGGCTGTAGTTTGAAGAACTGTGACAGTGTGATTTTCATACCGAGGCCCTA 960
DB 901 AAGCAAGGCTGTAGTTTGAAGAACTGTGACAGTGTGATTTTCATACCGAGGCCCTA 960
QY 961 GCTTCTTCACATGTTGTGGAACCCATCCTATGCTTCTCTGGAGCAATTTAA 1020
DB 961 GCTTCTTCACATGTTGTGGAACCCATCCTATGCTTCTCTGGAGCAATTTAA 1020
QY 1021 ACCTTGCCAGACGACACTACCTCTGTAGAGCAGAGGCTCAGCTCAAGATCTCTCC 1080
DB 1021 ACCTTGCCAGACGACACTACCTCTGTAGAGCAGAGGCTCAGCTCAAGATCTCTCC 1080
QY 1081 AAGGAAAGGAGAGTGAATTCATCTGTTTCACAGTGTGAGTCTTCAAGTTTTCAC 1140
DB 1081 AAGGAAAGGAGAGTGAATTCATCTGTTTCCACAGTGTGAGTCTTCAAGTTTTCAC 1140

QY	1141	TCGAGCTACACAGATGATAAAGCGCTTTTATACGTAATATACTTTTAAAGTT	1200
Db	1141	TCGAGCTACACAGATGATAAAGCGCTTTTATACGTAATATACTTTTAAAGTT	1200
QY	1201	ACACATTTTCAGATATATAAAGACGACCAATATTTGACAGTTTTTATGCTTGGAT	1260
Db	1201	ACACATTTTCAGATATATAAAGACGACCAATATTTGACAGTTTTTATGCTTGGAT	1260
QY	1261	TTTGCTGCTGCTCTTCTAGTTTGTAAGTTATAGCATATTAATAAATTTT	1320
Db	1261	TTTGCTGCTGCTCTTCTAGTTTGTAAGTTATAGCATATTAATAAATTTT	1320
QY	1321	TTTGTTTCATATTGANTGCTGCTAGGACGACCTGTGGCCAAAGTCTTAGTGGCTGAT	1380
Db	1321	TTTGTTTCATATTGANTGCTGCTAGGACGACCTGTGGCCAAAGTCTTAGTGGCTGAT	1380
QY	1381	GTCCTGCTGTAAGACCTAGAAAAAGGAACTGACATCTCCAGAGCGTGTAGTAATCAG	1440
Db	1381	GTCCTGCTGTAAGACCTAGAAAAAGGAACTGACATCTCCAGAGCGTGTAGTAATCAG	1440
QY	1441	TAAAGCTAGAAATGATATCCGACGCTGTTATGATATATCTCCGATCCCGGGAAC	1500
Db	1441	TAAAGCTAGAAATGATATCCGACGCTGTTATGATATATCTCCGATCCCGGGAAC	1500
QY	1501	GTCTTCCCTGTTCTTAAAGCGTATTTTGGCTAGAAAGTGGACATTATAACCAAGCC	1560
Db	1501	GTCTTCCCTGTTCTTAAAGCGTATTTTGGCTAGAAAGTGGACATTATAACCAAGCC	1560
QY	1561	AAATGGTATAGAAACCTCGCTTTTCAGTTTCAGAGTGGGTGATTTCAGCACCTAC	1620
Db	1561	AAATGGTATAGAAACCTCGCTTTTCAGTTTCAGAGTGGGTGATTTCAGCACCTAC	1620
QY	1621	AGTGTACAGCTCTGTATTAAAGTTGTTAATAAAGTACATGTTAACTTAAAAA	1680
Db	1621	AGTGTACAGCTCTGTATTAAAGTTGTTAATAAAGTACATGTTAACTTAAAAA	1680
QY	1681	AAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACGACACTGGAATTC	1737
Db	1681	AAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACGACACTGGAATTC	1737

1 FILING DATE: 11-JUN-1993
 2 PRIORITY APPLICATION DATA:
 3 APPLICATION NUMBER: 07/810782
 4 FILING DATE: 19-DEC-1991
 5 ATTORNEY/AGENT INFORMATION:
 6 NAME: Love, Richard B.
 7 REGISTRATION NUMBER: 34,659
 8 REFERENCE/DOCKET NUMBER: P0706P2PlC1
 9 TELECOMMUNICATION INFORMATION:
 0 TELEPHONE: 415/225-5530
 1 TELEFAX: 415/952-9881
 2 TELEX: 910/371-7168
 3 INFORMATION FOR SEQ ID NO: 3:
 4 SEQUENCE CHARACTERISTICS:
 5 LENGTH: 1737 base pairs
 6 TYPE: Nucleic Acid
 7 STRANDEDNESS: Single
 8 TOPOLOGY: linear
 9
 0 JS-08-805-478-3

Query Match	100.0%	Score 1737;	DB 4;	Length 1737;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1737; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	GAATTCACAGTGTGCTGGCGGCGCGGCCCAAGTACGCCACGAGGCGCTGAGTGTCTCCAGTA	60
Dp	1	GAATTCACAGTGTGCTGGCGGCGCGGCCCAAGTACGCCACGAGGCGCTGAGTGTCTCCAGTA	60
QY	61	GCACACCGCATCTGGAGAAACCAACGCGGTTACCATGAGAGGGATCGATATACACTTCAGAT	120
Dp	61	GCACACCGCATCTGGAGAAACCAACGCGGTTACCATGAGAGGGATCGATATACACTTCAGAT	120
QY	121	AACATACCCGAGAAATGGGCTCAGGSGGACATATGACTCCATCCATGGAAGAACCCCTTTTCGGT	180
Dp	121	AACATACCCGAGAAATGGGCTCAGGSGGACATATGACTCCATCCATGGAAGAACCCCTTTTCGGT	180
QY	181	GAAAGAAAATGCTAAATTTCAATAAAATCTTCCTGCGCCACCATCTACTGCATCATCTTCTTA	240
Dp	181	GAAAGAAAATGCTAAATTTCAATAAAATCTTCCTGCGCCACCATCTACTGCATCATCTTCTTA	240
QY	241	ACTGGCATTTGGGGCAATGGAATGGTATCTCTGTGTCATGGGTTACCAAGAAACTGAGA	300
Dp	241	ACTGGCATTTGGGGCAATGGAATGGTATCTCTGTGTCATGGGTTACCAAGAAACTGAGA	300
QY	301	AGCATACGGGACGAAGTACAGGCTGCACCTGTCAAGTGGGCGCACTCCTTTGTGCATCAGG	360
Dp	301	AGCATACGGGACGAAGTACAGGCTGCACCTGTCAAGTGGGCGCACTCCTTTGTGCATCAGG	360
QY	361	CTTCCTCTTGGGCGCATTTGATGCCGCTGGCAACTGTAATTTGGGAATCTCCTATGCAAG	420
Dp	361	CTTCCTCTTGGGCGCATTTGATGCCGCTGGCAACTGTAATTTGGGAATCTCCTATGCAAG	420
QY	421	GCAATCCATGTCTATCTACACAGTCAACCTTACACGACGTCTCTCATCTGGCGCTTCATC	480
Dp	421	GCAATCCATGTCTATCTACACAGTCAACCTTACACGACGTCTCTCATCTGGCGCTTCATC	480
QY	481	AGTGTGACCGGCTACCTGAGGCGATGCTCAAGCCCAACAGTACAGAGGCCAAGGAAGCTG	540
Dp	481	AGTGTGACCGGCTACCTGAGGCGATGCTCAAGCCCAACAGTACAGAGGCCAAGGAAGCTG	540
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Dp	541	TTGGCTGAAAAGGTGATCTATTTGGCGCTGTGATCCCTCCCTCGTGTGACTATTTCC	600
QY	601	GACTTCATCTTTGCCAACGTCAGTGAAGGACAGATATATCTGTACCCGCTTCTAC	660
Dp	601	GACTTCATCTTTGCCAACGTCAGTGAAGGACAGATATATCTGTACCCGCTTCTAC	660
QY	661	CCCATAGCATTTGGGGGTGTGTGTTCCATTTACAGACATCAATGGTGGCGCTTATCCG	720
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QY 721 CCTGATATGTCATCTGCTGCTATGTCATATTCATCTCCAAAGTGTCACTCCAG 780
      |||
      CCTGATATGTCATCTGCTGCTATGTCATATTCATCTCCAAAGTGTCACTCCAG 780
QY 781 GGCACCAAGAGCCGAGGCCCTCAAGACCACTCATCTCATCTGCTGCTGCTGCTG 840
      |||
      GGCACCAAGAGCCGAGGCCCTCAAGACCACTCATCTCATCTGCTGCTGCTGCTG 840
QY 841 TGTGGCTGCTTACTCATTTGGATGAGCATGTCAGTCCCTTCATCTCCGGAATATC 900
      |||
      TGTGGCTGCTTACTCATTTGGATGAGCATGTCAGTCCCTTCATCTCCGGAATATC 900
QY 901 AAGCAAGGCTGTGATTTGAGAACACTGTGCACAGTGGATTTTCATCAGCAGGCCCTA 960
      |||
      AAGCAAGGCTGTGATTTGAGAACACTGTGCACAGTGGATTTTCATCAGCAGGCCCTA 960
QY 961 GCTTCTTCCACTGTGTGTGTAACCCCATCTCATATGCTTCTGGAAGCAATTTAA 1020
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      GCTTCTTCCACTGTGTGTGTAACCCCATCTCATATGCTTCTGGAAGCAATTTAA 1020
QY 1021 ACCTCTCCAGCAGCAGCTACCTCTGTGAGAGAGGGTCCAGCCTCAAGATCTCTCC 1080
      |||
      ACCTCTCCAGCAGCAGCTACCTCTGTGAGAGAGGGTCCAGCCTCAAGATCTCTCC 1080
QY 1081 AAGGAAAGCGAGGTGACATTCATCTGTTCCACTGAGTGTGAGTTCAGATTTTAC 1140
      |||
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QY 1141 TCCAGCTAACACAGATGATAAAGCTTTTATACGATATAAATCTTTTAAAGTT 1200
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      TCCAGCTAACACAGATGATAAAGCTTTTATACGATATAAATCTTTTAAAGTT 1200
QY 1201 ACACATTTTCAGATATAAAGACTGACCAATATTTGACATTTTATGCTTGTGAT 1260
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      ACACATTTTCAGATATAAAGACTGACCAATATTTGACATTTTATGCTTGTGAT 1260
QY 1261 TTTTGTCTGTGTTCTTTAGTTTGTGAAGTTAAATGACATTTTATATAAATTTT 1320
      |||
      TTTTGTCTGTGTTCTTTAGTTTGTGAAGTTAAATGACATTTTATATAAATTTT 1320
QY 1321 TTTGTTTCAATGATGTGTGTCAGCAGAGACTGTGGCCAGTTCTTATGTTCTAT 1380
      |||
      TTTGTTTCAATGATGTGTGTCAGCAGAGACTGTGGCCAGTTCTTATGTTCTAT 1380
QY 1381 GTCTGTGTAGTAGTGTAGAAAAGGGAATGAACTTCAGAGCGTGTGTAATCAG 1440
      |||
      GTCTGTGTAGTAGTGTAGAAAAGGGAATGAACTTCAGAGCGTGTGTAATCAG 1440
QY 1441 TAAAGCTAGAAATGATCCCACTGTTATGATAGATTAATCTCTCATTCCTGGAAC 1500
      |||
      TAAAGCTAGAAATGATCCCACTGTTATGATAGATTAATCTCTCATTCCTGGAAC 1500
QY 1501 GTTTTCTCTTCTTAAGAGCTGATTTTGTGTAGAGATGGCACTATAACCAAGCCC 1560
      |||
      GTTTTCTCTTCTTAAGAGCTGATTTTGTGTAGAGATGGCACTATAACCAAGCCC 1560
QY 1561 AAGGTGTATAGAAATGCTGTTTTCAGTTTTCAGAGAGTGGTGTGATTTTCAGACCTAC 1620
      |||
      AAGGTGTATAGAAATGCTGTTTTCAGTTTTCAGAGAGTGGTGTGATTTTCAGACCTAC 1620
QY 1621 AGGTGACAGCTGTATATAGTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1680
      |||
      AGGTGACAGCTGTATATAGTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1680
QY 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGGCCCGCCAGCAGCTGGAATTC 1737
      |||
      AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGGCCCGCCAGCAGCTGGAATTC 1737
      Db 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGGCCCGCCAGCAGCTGGAATTC 1737
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RESULT 6
PCT-US94-06380-2
; Sequence 2, Application PC/TUS9406380
; GENERAL INFORMATION:

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APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: K. Jin Kim
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY DISORDERS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06380
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
FAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-06380-2
Query Match 100.0%; Score 1737; DB 5; Length 1737;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Db 361 CTTCCTTCCTGGGAGTTGATGCGGCAACTGGTACTTTGGGAACTTCTCATGCAAG 420
 QY 421 GCAGTCATATGTATCTACACAGTCAACCTCTACAGCAGTGTCTCTATCTGGCTTCATC 480
 Db 421 GCGAGTCATATGTATCTACACAGTCAACCTCTACAGCAGTGTCTCTATCTGGCTTCATC 480
 QY 481 ACTCTGAGCAGGCTACCTGGCCATCGTCACGCGCACCAAGAGTCAAGGCAAGAGCTG 540
 Db 481 ACTCTGAGCAGGCTACCTGGCCATCGTCACGCGCACCAAGAGTCAAGGCAAGAGCTG 540
 QY 541 TTGGCTGAAGAGTGGTCTATGTTGGCGCTCTGATCCCTGCTCTGCTGATTTCC 600
 Db 541 TTGGCTGAAGAGTGGTCTATGTTGGCGCTCTGATCCCTGCTCTGCTGATTTCC 600
 QY 601 GACTTCATCTTTGGCCAGCTCAGTGAAGCAGATGACAGATATATCTGTACCGCTTCTAC 660
 Db 601 GACTTCATCTTTGGCCAGCTCAGTGAAGCAGATGACAGATATATCTGTACCGCTTCTAC 660
 QY 661 CCCAATGACTTGGGCTGGTGTGTCAGATTCCAGTTCACGACATATGTTGGCTTATCTG 720
 Db 661 CCCAATGACTTGGGCTGGTGTGTCAGATTCCAGTTCACGACATATGTTGGCTTATCTG 720
 QY 721 CCTGTATATGTCATCTCTGCTGCTATTCATTCATTCATTCATTCATTCATTCATTC 780
 Db 721 CCTGTATATGTCATCTCTGCTGCTATTCATTCATTCATTCATTCATTCATTCATTC 780
 QY 781 GCGCAGCAGAGCGCAGAGCGCTCAAGACACAGTATCTCTGCTGCTTCTTCTGCGC 840
 Db 781 GCGCAGCAGAGCGCAGAGCGCTCAAGACACAGTATCTCTGCTGCTTCTTCTGCGC 840
 QY 841 TGTGGCTGCTTACTACATTTGGGATGACATGACATGACATGACATGACATGACATG 900
 Db 841 TGTGGCTGCTTACTACATTTGGGATGACATGACATGACATGACATGACATGACATG 900
 QY 901 AAGCAAGGCTGTGATTTGAGAACACTGTGCACAACTGATTTCCATCCAGCGCCCTA 960
 Db 901 AAGCAAGGCTGTGATTTGAGAACACTGTGCACAACTGATTTCCATCCAGCGCCCTA 960
 QY 961 GCTTTCTTCCATCTGTTGTGAACCCCATCTCTATGCTTCTTCTTGGAGCCAAATTTAA 1020
 Db 961 GCTTTCTTCCATCTGTTGTGAACCCCATCTCTATGCTTCTTCTTGGAGCCAAATTTAA 1020
 QY 1021 ACCTTGCCGACAGCAGCTCACTCTGTGAGAGAGGCTCCAGCTCAAGATCTCTCC 1080
 Db 1021 ACCTTGCCGACAGCAGCTCACTCTGTGAGAGAGGCTCCAGCTCAAGATCTCTCC 1080
 QY 1081 AAAGGAAAGCGAGGTGACATTCATCTGTTCCACTGAGTCTGAGTCTTCAAGTTTCA 1140
 Db 1081 AAAGGAAAGCGAGGTGACATTCATCTGTTCCACTGAGTCTGAGTCTTCAAGTTTCA 1140
 QY 1141 TCCAGTACACAGATTAAGACTTTTATATGATTAATTAATTAATTAATTAAGTT 1200
 Db 1141 TCCAGTACACAGATTAAGACTTTTATATGATTAATTAATTAATTAATTAAGTT 1200
 QY 1201 ACACATTTTTCAGATTAAGACTGACCAATTTTACAGTTTATGCTTGTGGAT 1260
 Db 1201 ACACATTTTTCAGATTAAGACTGACCAATTTTACAGTTTATGCTTGTGGAT 1260
 QY 1261 TTTTGTCTGTCTTCTTATGTTTGTGAAGTTTAAATTGACTTATTAATAAATTTT 1320
 Db 1261 TTTTGTCTGTCTTCTTATGTTTGTGAAGTTTAAATTGACTTATTAATAAATTTT 1320
 QY 1321 TTTGTTTATATGATGTGTCTAGGACAGACCTGTGGCCAAAGTTCTTATGCTGTAT 1380
 Db 1321 TTTGTTTATATGATGTGTCTAGGACAGACCTGTGGCCAAAGTTCTTATGCTGTAT 1380
 QY 1381 GTCTGCTGATGAGCTGTGAAAAGGAACTGAACTTCAGAGCTGTAGTGAATCAAG 1440
 Db 1381 GTCTGCTGATGAGCTGTGAAAAGGAACTGAACTTCAGAGCTGTAGTGAATCAAG 1440
 QY 1441 TAAAGCTAGAAATGATCCAGCTGTTTATGATATGATATATCTCCATCCCGTGAAC 1500
 Db 1441 TAAAGCTAGAAATGATCCAGCTGTTTATGATATGATATATCTCCATCCCGTGAAC 1500

QY 1501 GTTTTCTGTTCTTAACAGCTGATTTGCTGTAGACATGCGACTTAACCAAGCCC 1560
 Db 1501 GTTTTCTGTTCTTAACAGCTGATTTGCTGTAGACATGCGACTTAACCAAGCCC 1560
 QY 1561 AAAGTGTATAGAAATGCTGTTTTCAGTTTTCAGAGTGGTGTGATTTACGACCTAC 1620
 Db 1561 AAAGTGTATAGAAATGCTGTTTTCAGTTTTCAGAGTGGTGTGATTTACGACCTAC 1620
 QY 1621 AGTGTACAGCTCTTGTATTAAGTTGTTAATAAGTACATGTTAACTTAACCAAGAAA 1680
 Db 1621 AGTGTACAGCTCTTGTATTAAGTTGTTAATAAGTACATGTTAACTTAACCAAGAAA 1680
 QY 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACGACACTGGAATTC 1737
 Db 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACGACACTGGAATTC 1737

RESULT 7

US-08-153-848-45
 ; Sequence 45, Application US/08153848
 ; Patent No. 5759804
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schweikert, Vicki L.
 ; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/153,848
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/977,452
 ; FILING DATE: 17-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5759804and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 31794
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 45:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1317 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 201..1211
 ; US-08-153-848-45

Query Match 64.4%, Score 1118.2, DB 3, Length 1317,
 Best Local Similarity 99.6%, Pred. No. 1.5e-224;
 Matches 1131, Conservative 0, Mismatches 3, Indels 1, Gaps 1.

106 ATATACCTTCAGATTAACACCGAGAAATGGGCTCAGGGGACTATGACTCCATGAAG 165
171 ATATACCTTCAGATTAACACCGAGAAATGGGCTCAGGGGACTATGACTCCATGAAG 230
166 GAACCTGTTTCGTCGAGAAATGCTAATTTCAATAAATCTCTGCGCCACCATCTAC 225
231 GAACCTGTTTCGTCGAGAAATGCTAATTTCAATAAATCTCTGCGCCACCATCTAC 290
226 TCATCATCTTTCTTAAGTCGATTTGGGCAATGATTTGTCATCTCTGTCATGGTTAC 285
291 TCATCATCTTTCTTAAGTCGATTTGGGCAATGATTTGTCATCTCTGTCATGGTTAC 350
286 CAGAAGAACTGAGAAGCATGAGCGAGTAGACAGGCTCAGCTGTCATGGCGGACCTC 345
351 CAGAAGAACTGAGAAGCATGAGCGAGTAGACAGGCTCAGCTGTCATGGCGGACCTC 410
346 CTCCTTGTTCATCAGGCTTCCCTTCTGGGAGTTGATGCCGTGGCAAACTGTACTTTGG 405
411 CTCCTTGTTCATCAGGCTTCCCTTCTGGGAGTTGATGCCGTGGCAAACTGTACTTTGG 470
406 AACTTCCCTTGAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 465
471 AACTTCCCTTGAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 530
466 ATCTGAGCCTTATCAGTGTGAGACCGCTACCTGAGCCATGTCACGCGCCACCAAGTAC 525
531 ATCTGAGCCTTATCAGTGTGAGACCGCTACCTGAGCCATGTCACGCGCCACCAAGTAC 590
526 AGGCCAAGAACTGTTGGCTGAAAAAGTGTATGTTGGGCTGTGATGCTGCTGCTGCTC 585
591 AGGCCAAGAACTGTTGGCTGAAAAAGTGTATGTTGGGCTGTGATGCTGCTGCTGCTC 650
586 CTGCTGACATCTCCGACCTTCACTTTTGGCAAGTCAGTACGAGGAGATGACAGATATAC 645
651 CTGCTGACATCTCCGACCTTCACTTTTGGCAAGTCAGTACGAGGAGATGACAGATATAC 710
646 TGTGACCGCTTACCCCAATGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 705
711 TGTGACCGCTTACCCCAATGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 770
706 GTTGGCCTTATCTGCTGT 765
771 GTTGGCCTTATCTGCTGT 830
766 CTGTACACCTCAAGGGCCACGAGAGGCGCAAGGCGCTCAAGACCAATCATCTCCATC 825
831 CTGTACACCTCAAGGGCCACGAGAGGCGCAAGGCGCTCAAGACCAATCATCTCCATC 890
826 CTGCTTCTTCTGCTGT 885
891 CTGCTTCTTCTGCTGT 950
886 CTCTTGGAAATATATACAGCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 945
951 CTCTTGGAAATATATACAGCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1010
946 ATACCCGAGGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1005
1011 ATACCCGAGGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1070
1006 GGAGCCAAATTTAAACCTGTGCCAGCAGCAGTACCTCTGTGTGTGTGTGTGTGTGTGT 1065
1071 GGAGCCAAATTTAAACCTGTGCCAGCAGCAGTACCTCTGTGTGTGTGTGTGTGTGTGT 1130
1066 CTCAGATCTCTCCAAAGGAGGAGGTGACATTCATCTGTGTGTGTGTGTGTGTGTGTGT 1125
1131 CTCAGATCTCTCCAAAGGAGGAGGTGACATTCATCTGTGTGTGTGTGTGTGTGTGTGT 1190
1126 TCTTCAAGTTTCACTCCAGCTACAGATGTAAAGACTTTTCTTCTTCTTCTTCTTCTTCT 1185
1191 TCTTCAAGTTTCACTCCAGCTACAGATGTAAAGACTTTTCTTCTTCTTCTTCTTCTTCT 1249
1186 ACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1240

Db 1250 ACCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1304

RESULT 8
PCT-US93-11153-45
Sequence 45, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schelkard, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Marshall
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 201..1211
PCT-US93-11153-45

Query Match 64.4%; Score 118.2; DB 5; Length 1317;
Best Local Similarity 99.6%; Pred. No. 1.5e-224;
Matches 1131; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

106 ATATACCTTCAAGTAACTACACCGAGAAATGGGCTCAGGGGACTATGACTCCATGAAG 165
171 ATATACCTTCAAGTAACTACACCGAGAAATGGGCTCAGGGGACTATGACTCCATGAAG 230
166 GAACCTGTTTCGTCGAGAAATGCTAATTTCAATAAATCTCTGCGCCACCATCTAC 225
231 GAACCTGTTTCGTCGAGAAATGCTAATTTCAATAAATCTCTGCGCCACCATCTAC 290
226 TCATCATCTTTCTTAAGTCGATTTGGGCAATGATTTGTCATCTCTGTCATGGTTAC 285
291 TCATCATCTTTCTTAAGTCGATTTGGGCAATGATTTGTCATCTCTGTCATGGTTAC 350
286 CAGAAGAACTGAGAAGCATGAGCGAGTAGACAGGCTCAGCTGTCATGGCGGACCTC 345
351 CAGAAGAACTGAGAAGCATGAGCGAGTAGACAGGCTCAGCTGTCATGGCGGACCTC 410


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: Sequence 3, Application PC/TUS9503032
: GENERAL INFORMATION:
: APPLICANT: Repligen Corporation
: APPLICANT: the Trustees of Boston University
: TITLE OF INVENTION: ANTIBODIES TO INTERLEUKIN-8 RECEPTORS AND
: TITLE OF INVENTION: METHODS OF USE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: COMPUTER: IBM PS/2 Model 502 or 55SX
: OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
: SOFTWARE: WordPerfect (Version 5.0)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/03032
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/237,937
: FILING DATE: 02-MAY-94
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/210,250
: FILING DATE: 15-MAR-94
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/803,842
: FILING DATE: 09-DEC-91
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/726,606
: FILING DATE: 09-JUL-91
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/685,101
: FILING DATE: 10-APR-91
: ATTORNEY/AGENT INFORMATION:
: NAME: Fasse, J. Peter
: REGISTRATION NUMBER: 32,983
: REFERENCE/DOCKET NUMBER: 04/66/015WO1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-5070
: TELEFAX: (617) 542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1373
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: PCT-US95-03032-3

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Query Match 11.6%; Score 201.2; DB 5; Length 1373;
Best Local Similarity 54.8%; Pred. No. 11e-33;
Matches 467; Conservative 0; Mismatches 373; Indels 12; Gaps 3;

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QY 175 TTCGCTGAAGAAATGCTAATTTCAATAAATCTCTGCGCCACGATCACTGCATC 234
DB 179 TGCCTGCTGAATCTCTGAAACACAGTATGTGCTCATCACTATATCTGTC 238
QY 235 TTCTTACTGCGATTGTGGCAATGATGTGTCATCTCTGTCATCGGTTACGAGAA 294
DB 239 TTCTGCTGCTGCTGCTGCGCACTCCCTGCTGATCTGCTCATCTGTACACCGGAG 298
QY 295 CTGAGACGATGAGGACGATGACGCTGACGCTGAGTGGCGACCGCTCTTGTG 354
DB 299 ACCTGCTGCTGACGACGATGACGCTGACGCTGACGCTGACGCTGACGCTGACG 358
QY 355 ATCAGCTTCCCTTCTGGCGAGTTGATGCGCTGGCAAACTGTACTTTGGGAACTTCT 414

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DB 359 ACCACCTTGCCACTCTGCGCGCCGCTCCAAAGGTGACGCGCTGAGCTTTGCGACGCCCC 418
QY 415 TGCAGGACGATCCATCTGATCACTACAGCTCAACCCCTACAGAGTGTCTCATCTGCGC 474
DB 419 TGTAAAGTGTCTGCTCTGTGTAAGAACTCACTTCTACAGCGGAACTCTGCTGCGC 478
QY 475 TTCACTAGCTGTGACCGCTTACCTGCGCATGTCACGCGCCACCAACGATGAGGCGAA 534
DB 479 TGCATCAGTGTGACCGCTTACCTGCGCATGTCACGCGCCACCAACGATGATGCAAG 538
QY 535 AAGCTGTGCTGAAAGAGTGTCTATGTGGCGCTGTGATCCCTGCTGCTGACT 594
DB 539 CGCCACTTG--GTCAAGTATATGCTTAAGCAATGTGGGAGTGTCTTGTACTCTGCT 595
QY 595 ATTCCGACTTCATCTTGTCCCAAGCTGAGTGAAGCA--GATGACAGATATATCTG-- 648
DB 596 CTGCCATCTTACTTTCGATATGCAATCTTCCACCAATTCAGCGCCGCTGCTGAT 655
QY 648 --TGACCGCTTCTACCCCAATGACTTGTGGTGTGTGTGTCAGTTTCAGACATCATG 705
DB 656 GAGACATGTGGGACAGACGCTGCAAAATGGGCGCATGTGCTGCGGATCTGCTGACT 715
QY 706 GTTGGCTTATCTGCTGCTGATGTGATCTCTGCTCTGATGCTATATCATCTTCCAG 765
DB 716 TTGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 775
QY 766 CTGTCACTCTCAAGGCGCACAGGCGCAAGGCGCAAGGCGCTCAAGACGATCATCTCAT 825
DB 776 CTGTTCAGGCGCCACAGTGGGCGCAAGGCGCAAGGCGCTCATCTTCCCTGCTG 835
QY 826 CTGGCTTCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885
DB 836 CTGATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895
QY 886 CTCTCGGAATATATCAAGCAAGGCTGTGATGTGGAACACTGCTGCAAGTGTGCTC 945
DB 896 AGGACCCAGCTGATCAGAGAGCTGTGAGGCGCCGCAATGACATTTGACCGGCGCTG 955
QY 946 ATCAGGAGGCGCTGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
DB 956 GCGACGAGATTTCTGGGCTTCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTG 1015
QY 1006 GGAGCCAAATTT 1017
DB 1016 GGGCAAAAGTTT 1027

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RESULT 12
PCT-US92-02977-1
: Sequence 1, Application PC/TUS9202977
: GENERAL INFORMATION:
: APPLICANT: Navarro, Javier et al.
: TITLE OF INVENTION: INTERLEUKIN-8 RECEPTORS AND
: TITLE OF INVENTION: RELATED MOLECULES AND
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: COMPUTER: IBM PS/2 Model 502 or 55SX
: OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
: SOFTWARE: WordPerfect (Version 5.0)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/02977
: FILING DATE: 19920410
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:

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Query Match	11.3%	Score 196.8	DB 1	Length 1933
Best Local Similarity	53.9%	Pred. No. 9.8e-33		
Matches 455	Conservative 0	Mismatches 377	Indels 12	Gaps 2
<p>PRIOR APPLICATION DATA: 07/810782</p> <p>APPLICATION NUMBER: 07/810782</p> <p>FILING DATE: 19-DEC-1991</p> <p>PRIOR APPLICATION DATA: 07/677211</p> <p>APPLICATION NUMBER: 07/677211</p> <p>FILING DATE: 29-MAR-1991</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Love, Richard B</p> <p>REGISTRATION NUMBER: 34,659</p> <p>REFERENCE/DOCKET NUMBER: 706P2</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 415/225-5530</p> <p>TELEFAX: 415/952-9881</p> <p>TELEX: 910/371-7168</p> <p>INFORMATION FOR SEQ ID NO: 1:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 1933 nucleotides</p> <p>TYPE: Nucleic Acid</p> <p>STRANDEDNESS: Single</p> <p>TOPOLOGY: Linear</p> <p>US-08-076-093A-1</p>				
183	AGAAATGCTAATTCAATAAATTTCTCCGCCACACATCTACTCCATCATCTTTTAAAC	242		
146	AGAACTGAGACACTCAACAAATATGTTGATCATGCGCTATGCCCTAATGTTCTGCT	205		
243	TGGCATTGTGGCAATGATGTTGGTCATGCTGATGGTTACGAGAAGAACTGAGAG	302		
206	GACCTGCTGGGAAATCCCTGCTGATGCTGCTATCTATACGACAGGCTGGCGGCTC	265		
303	CATGACGAGCAAGTACAGGCTGACACTCTACAGTGGCCGACCTCTCTTTTATCAAGCT	362		
266	CGTCACTGATGTCATCTGCTGAACCTGCGCTTGGCCGACCTACTCTTTCCCTGACCTT	325		
363	TCCCTCTGGGCAAGTATGATGCCGTGCAAACTGGTACTTTGGGAACTTCTATGCAAGG	422		
326	GCCCATCTGGGCGGCTCCAAAGTAAATGCTGATTTTGGACATTTCTGTGCAAGGT	385		
423	AGTCATGTCATCTACAGAGTCAACCTCTACAGAGTGTCTCATCTCTGCTTTCATCAG	482		
386	GGTCTACCTCTGAGGAAGATCACTTCTACAGTGGCATCCTGCTGTTGGCTGATCAG	445		
483	TCGAGACGCTACCTGGGCACTGTCACAGCCACCAACAGTACGAGGCAAGGAGCTGTT	542		
446	TGTGGACGCTTACCTGGGCACTGTCACAGCCACCAAGTACGAGGCAAGGAGCTGTT	505		
543	GAGTGAAGAGTGTCTATGTTGGGCTGATGCTTCCCTGCTGCTGATCTTCCGCA	602		
506	G---GTCAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	562		
603	CTTCACTTTTGGCAAGTCACTGAGGAGCATGACAGATATATCTGT-----GACCG	653		
563	CTTCTCTTTTCCGCGAGGCTTACCATCCAAACAAATTCAGTCCAGTTGCTATGAGTCT	622		
654	CTTCTACCCCATGACTGTTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	713		
623	GGGAATGACACGAGAAATGCGGATGTTGCTGCGGATCTCTCTACACCTTTGGCTT	682		
714	TATCCGCTGCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	773		
683	CATCGGCGGCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	742		
774	CTTCAAGGAGCAGCAAGGAGGCTTCAAGACCAAGTACGCTATCTGCTGCTGCTT	833		
743	GAGCCACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	802		
834	CTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	893		

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 14, 1999, 09:52:22 : Search time 284.76 Seconds
(without alignments)
12032.205 Million cell updates/sec

Title: US-09-104-063-3

Perfect score: 1737
Sequence: 1 GAATTCAGTGTCTGCGG.....CCGCACACATGGAATTC 1737

Scoring table: IDENTITY_NUC

Searched: 2546578 seqs, 986266752 residues

Database :

EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
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14: em_est14:*
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18: em_est18:*
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49: em_est49:*
50: em_est50:*
51: em_est51:*
52: em_est52:*
53: em_est53:*

54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	670.8	38.6	786	37	AA707668	AA707668 z129f12.s
2	646.8	37.2	792	38	AA781110	AA781110 a123e10.s
3	606.6	34.9	693	36	AA634211	AA634211 ac72b06.s
4	601.4	34.6	657	47	AI493618	AI493618 th39e07.x
5	592.4	34.1	651	36	AA634201	AA634201 ac72b07.s
6	589	33.9	589	40	AA935648	AA935648 cp27c09.s
7	567.8	32.7	599	33	AA411265	AA411265 zv24f06.t
8	546.8	31.5	593	35	AA576017	AA576017 nm57f04.s
9	544.8	31.4	556	38	AA743645	AA743645 ny24g09.s
10	539	31.0	539	36	AA610463	AA610463 np97b09.s
11	514.6	29.6	521	34	AA479467	AA479467 zv17f10.r
12	511.8	29.5	555	38	AA747545	AA747545 nx85g08.s
13	506	29.1	583	29	AA148282	AA148282 zc45e12.s
14	501.2	28.9	536	38	AA804282	AA804282 nw30h06.s
15	501	28.8	501	33	AA426644	AA426644 zv47h11.s
16	492.2	28.3	524	44	AI249788	AI249788 qx51c10.x
17	491.4	28.3	509	38	AA760743	AA760743 n210b09.s
18	490.8	28.3	531	46	AI434652	AI434652 t134d02.x
19	485	27.9	504	43	AI159856	AI159856 qb51c09.x
20	483.4	27.8	535	41	AI022030	AI022030 cw72a11.x
21	473.8	27.3	524	48	AI583169	AI583169 tr98d12.x
22	470.6	27.1	538	39	AA824607	AA824607 cc83f08.s
23	470	27.1	470	33	AA426566	AA426566 zv47h11.r
24	464.6	26.7	473	44	AI300764	AI300764 qp50c09.x
25	462.8	26.6	482	41	AI002547	AI002547 q990e01.s
26	458.2	26.4	483	45	AI344724	AI344724 qp04h09.x
27	456.8	26.3	552	37	AA731086	AA731086 nw68a05.x
28	448.6	25.8	455	44	AI300807	AI300807 qn47b03.s
29	446.8	25.7	537	34	AA479357	AA479357 zv17f10.s
30	439.4	25.3	456	32	AA354393	AA354393 EST52864
31	434.8	25.0	494	31	AA284569	AA284569 zt22e05.r
32	433.6	25.0	639	39	AA816049	AA816049 vr14h02.r
33	429.8	24.7	465	45	AI370816	AI370816 fa58c10.x
34	428	24.6	428	30	AA259199	AA259199 nc17b08.r
35	424.4	24.4	793	29	AA182270	AA182270 mt83f01.r
36	424.4	24.1	419	44	AI284206	AI284206 q126h07.x
37	416.4	24.0	475	43	AI193140	AI193140 q40f12.s
38	415.4	23.9	417	45	AI358446	AI358446 qx19c11.x
39	415	23.9	454	31	AA284857	AA284857 zt22e05.s
40	413	23.8	437	50	AI675038	AI675038 wc21e10.x
41	409	23.5	409	34	AA490436	AA490436 aa51e04.r
42	404	23.3	405	50	AI682902	AI682902 wc69g07.x
43	401	23.1	401	49	AI660355	AI660355 we62b07.x
44	393.4	22.6	437	40	AA934663	AA934663 co071c08.s
45	393	22.6	393	33	AA386000	AA386000 EST95758

ALIGNMENTS

RESULT 1
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LOCUS AA707668
DEFINITION z129f12.s1 Soares_fetal_liver-spleen_INFUS_S1 Homo sapiens cDNA
clone IMAGE:451727.3' similar to gb:L06797 PROBABLE G
PROTEIN-COUPLED RECEPTOR LCRI HOMOLOG (HUMAN);, mRNA sequence.
ACCESSION AA707668
NID g2717586

Db	621	GANCAAGAGTCCACACTTCAGAGACTCTCCAAAGGAGCCAAAGTGGACATCTATCTGT	562
QY	1110	TTCCAGCTGAGTGTGAGTCTTCAAGTTTTCACATCCAGCTAACACAGATGTAAAGACTTTT	1169
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QY	1170	TTTTATAGCATAAATAACTTTTTTTTAAAGTTCACATTTTTCAGATATAAAGACTGACC	1229
Db	502	TTTTATAGCATAAATAACTTTTCTTAAAGTTCACATTTTTCAGATATAAAGACTGACC	443
QY	1230	AATATTGTACAGTTTTCATTCGTTGGATTTTGTCTGTGTTCTTAAAGTTTGTG	1289
Db	442	AATATTGTACAGTTTTCATTCGTTGGATTTTGTCTGTGTTCTTAAAGTTTGTG	383
QY	1290	AAGTTTAATTGACTTATTTATATATTAATTTTTTTTGTTCATATGTAGTGTGACCA	1349
Db	382	AAGTTTAATTGACTTATTTATATATTAATTTTTTTTGTTCATATGTAGTGTGACCA	323
QY	1350	GGACCTGTGGCCAAAGTTCTTAAGTGTCTGTATCTCTGCTGTGTAGACTGTAGAAAAGGAA	1409
Db	322	GGACCTGTGGCCAAAGTTCTTAAGTGTCTGTATCTCTGCTGTGTAGACTGTAGAAAAGGAA	263
QY	1410	CTGACATCTCCGACGCGTGTAGTGAATCAGCGTAAGCGTAGAATATATCCACGCTGTTA	1469
Db	262	CTGACATCTCCGACGCGTGTAGTGAATCAGCGTAAGCGTAGAATATATCCACGCTGTTA	203
QY	1470	TGCATAGATAAATCTCTCCATCTCCGTTGGAACTTTTTCCTGTCTTAAAGCTGATTTTG	1529
Db	202	TGCATAGATAAATCTCTCCATCTCCGTTGGAACTTTTTCCTGTCTTAAAGCTGATTTTG	143
QY	1530	CTGTGAAGATGGACACTTATAAACCAAGGCCAAAGTGTATAGAAATCTGTGTTTTTCAG	1589
Db	142	CTGTGAAGATGGACACTTATAAACCAAGGCCAAAGTGTATAGAAATCTGTGTTTTTCAG	83
QY	1590	TTTTTACGAGTGTGGTTGATTTCAGACACCTACAGTGTACAGTCTTATTAAGTTTAT	1649
Db	82	TTTTTACGAGTGTGGTTGATTTCAGACACCTACAGTGTACAGTCTTATTAAGTTTAT	23
QY	1650	AAAAGTACATGTTAACTTAA 1671	
Db	22	AAAAGTACATGTTAACTTAA 1	
RESULT 4			
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LOCUS	AI493618	657 bp	mRNA
DEFINITION	U9907.1 x1 NC1-CGAP_Pan1 Homo sapiens cDNA clone IMAGE:210676	EST	30-MAR-1999
	similar to g9:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1		
	HOMOLO (HUMAN);, mRNA sequence.		
ACCESSION	AI493618		
NID	94394621		
VERSION	AI493618.1	GI:4394621	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 657)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997)		
	On May 18, 1998 this sequence version replaced gi:3137291.		

Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LINTL at:
www-bio.1ml.gov/dbip/image/image.html

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Insert Length: 1615   Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 410.
Location/Qualifiers
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FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2120676"
/clone_1_id="NCI CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1: SalI;
Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11348-013"

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BASE COUNT	232 a	130 c	109 g	184 t	2 others
ORIGIN					

Query Match:	34.6%	Score 601.4:	DB 47:	Length 657:
Best Local Similarity:	98.2%	Pred. No. 8.6e-100:		
Matches 649, Conservative	0:	Mismatches 8:	Indels 4:	Gaps 4:

Oy	1017	TAAACCTCCTCCAGCAGCAGCACTCAGCTCTGTGACAAGAGGTCCAGCCTCAAAATCT	1076
Db	657	TTAAACTCTGCCAGCAGC-ACTCAGCTCTGTGACAGAGAGGTGAGCCNTCAAGT-CT	600
Oy	1077	CTCAAGAGAAAGCGAGGTGACATTCATCTGTTCCATGAGTCTGAGTCTTCAAGTT	1136
Db	559	CTCCAAAGAAAGGAGGTGAGAA-TCATCTGTTTCCATGAGTCTGAGTC-TCAAGTT	542

Oy 1137 TCATCCAGCTAACACGATGTAAAGACTTTTTTTTATACATAAATCACTTTTTTTA 1196
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 541 TCACTCAGCTAACACGATGTAAAGACTTTTTTTTATACATANATACTTTTTTTTA 482

07 1197 AGTACACATTTTCACATATAAAGACGACCAATATTGTACAGTTTATGCTGTT 1256
 Db 481 AGTTACACATTTTCACATATAAAGACGACCAATATTGTACAGTTTATGCTGTT 422

0Y	1317	TTTTTTTGGTTTCATATGAGTGGTGGTTTGAAGCAGACCTGGTGGCCCAAGTCTTACCTGCT	1317
0Y	125/	GGATTTTTCGCTCTGTGTTCTTAGTTAGTTTGGCAATTAAATGGACTTATTTATTAAT	1318
Db	421	GGATTTTTCGCTCTGTGTTCTTAGTTTGGCAATTAAATGGACTTATTTATTAAT	362

Db	TTTTTTGTTTCATATTGAAGTGTGTCTACGGCAGGCACTGTGGCCAAGTTCTTAAGTGCT	302
Dy	GTAGTCTCGTGGTAGGAAAGGGAACGTGCACATTTCCAGAGCGGTACTGAAT	1438

Db 301 GTATGTCTCGTGGTAGACTGTAGAAAAAGGAACCTGAACATTCCAGAGCGTTAAGTGAAT 242
 97 1437 CACGTAAGCGTAGAATGATCCCGACGCTTTATGATAGATATCTCCATTCCTCCGCTG 1498

Db 241 CACGTAAAGCTAGAAATGATCCCGAGGTGTTATGCATGAGTAATCTCCATTCCTCCG 182

Oy 1497 GAACGTTTTCTGTCTTCTTAAGACGCGATTTTCTCTAGAGAGTGGCACTTAAACAAA 1556

Db 181 GAACGTTTTTCCTGTTTAAAGCAGGATTTTGCCTGTAACAAATGGCACTTAATAACAAA 122

Gy 1557 GCCCAAGTGTATAGAAATGCTGTTTTCAGTTTTCAGGAGTGGCTGATTAGACAC 1616

Db 121 GCCAAGGTGGTATAGAAATCGTGGTTTTTCAGTCTTCAGAGAGTGGGTGATTTCAGCAC 62

Qy 1617 CTACAGTGTACAGCTCTGTATTAGTTGTTAAATAAAAGTACATGTTAAACTTAAAAAAA 1678

DB 01 CTAAGGCTACAGCTCTGTTTAAAGTGGTTAAATAAAGTACATGTTTAACTTAAAAAA 2

QY 1677 A 1677

DB 1 A 1

RESULT	5				
AA634201/c					
LOCUS	AA634201	651 bp	mrna	EST	21-Oct-1997
DEFINITION	ac72807.s1 Stratiagene lung (#937210) Homo sapiens cDNA clone				
IMAGE:	868116 3' similar to gb:106797 PROBABLE G PROTEIN-COUPLE				
RECEPTOR	LCR1 HOMOLOG (HUMAN)). mRNA sequence.				
ACCESSION	AA634201				
NID	92557415				
VERSION	AA634201.1	GI:2557415			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
	Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 651)				
AUTHORS	Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S. Kizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Stepec,M., Tan,F., Thiesing,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.				
TITLE	WashU-NCI human EST Project				
JOURNAL	Unpublished (1997)				
COMMENT	On Sep 12, 1996 this sequence version replaced gi:1393737.				

CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available royalty-free through LINL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: -40mls fwd. ET from Amersham
 High quality sequence stop: 413.
 Location/Qualifiers

```

FEATURES
Source
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:868116"
/clone_lib="Stratagene Lung (#537210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: lung; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
0.190 dt. normal lung. Average insert size: 1.0 kb;
UniZAP XR Vector: -5' adaptor sequence: 5' GAATTCGACGACGAG
3' -3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'"
BASE COUNT
230 a 130 c 112 g 179 t
ORIGIN

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	Query Match	34.1%	Score 592.4	DB 36	Length 651
	Best Local Similarity	96.3%	Pred. No. 3.7e-98		
	Matches 628	Conservative	0	Mismatches 21	Indels 3; Gaps
QY	1020	AACCTCTGCCAGCAGCACACTCACTCCTGTGTGACAGAGGGTCCAGCGCTTCAMATCCTCTC			1079
Dd	649	AAACCTCTGCCAGCAGCGCACTTACACTTTGTGACACA -GTCACAGCTTAATCTCTC			591
QY	1080	CAAAGGAAGCCGAGGTGACATTCATCTGTTCCACTGAGTGCTGACGTCTTCAAAGTTTTCA			1139
Dd	590	CAA--GGAAAGCAGTGCAGCATTCATCTGTTCCACTGAGTGCTGAGTCTTCAAAGTTTTCA			533
QY	1140	CTCCAGTAGCACAGATGTAAAGACTTTTTTTTATAGCATATAATPACTTTTTTAGT			1199
Dd	532	CTCCAGTAGCACAGATGTAAAAAGACTTTTTTTTATAGCATATAATPACTTTTTTAGT			473
QY	1200	TACACATTTTTCAGATATAAAGAAGCTGACCATAATTGTACAGTTTTTATTTGCTTTGGA			1259
Dd	472	TACACATTTTTCAGATATAAAGAAGCTGACCATAATTGTACAGTTTTTATTTGCTTTGGA			413
QY	1260	TTTTTGCTCTGTGTTCTTTAGTTTTTTGTGAAGTTAATGTACTATTATATAAATTTT			1319

Db	412	TTTTTGCTGGTTCCTTTACTTTTTTGTGAAGTTAATTACTTATTTATATAAATTT	353
QY	1320	TTTTGTTTCATATGATGATGTGTCTAGGACGAGCCTGTGGCCAAGTTCCTAATGTCGTGA	1379
Db	352	TTTTGTTTCATATGATGATGTGTCTAGGACGAGCCTGTGGCCAAGTTCCTAATGTCGTGA	293
QY	1380	TGTCCTGCTGGTAGGACTGTAGAAAAAGGAACTGAAACATTTCCAGACGCTGTAGTAAATCAC	1439
Db	292	TGTCCTGCTGGTAGGACTGTAGAAAAAGGAACTGAAACATTTCCAGACGCTGTAGTAAATCAC	233
QY	1440	GTTAAGCTGAATATGATCCCCAGCTGTTATATCATATGATATATCTCTCATTCCTCCGTGAA	1499
Db	232	GTTAAGCTGAATATGATCCCCAGCTGTTATATCATATGATATATCTCTCATTCCTCCGTGAA	173
QY	1500	CGTTTTTCCTGTTCTTAAAGCCTGATTTTGCCTGTAGAAGATGGCACTTATTAACCAAGCC	1559
Db	172	CGTTTTTCCTGTTCTTAAAGCCTGATTTTGCCTGTAGAAGATGGCACTTATTAACCAAGCC	113
QY	1560	CAAAAGTGTATAGAAATGCTGTTTTTTCAGTTTTCAGSAGTGGGTTGATTTTCAGACCTGA	1619
Db	112	CAAAAGTGTATAGAAATGCTGTTTTTTCAGTTTTCAGSAGTGGGTTGATTTTCAGACCTGA	53
QY	1620	CAGGTACACAGTCTTGATTAATGTTGTTATPAAAAAGTACATTTTAACTTAAA	1671
Db	52	CAGGTACACAGTCTTGATTAATGTTTATATAAAGTACATTTTAACTTAAA	1

RESULT	6	
LOCUS	AA935648/c	
DEFINITION	AA935648 589 bp mRNA	EST 07-JUL-1998
LOCUS	OP22C09.s1 Soares_NFL_T_GRC_S1 Homo sapiens CDNA clone	
DEFINITION	IMAGE:5578064 3, similar to gb:D06797 PROBABLE G PROTEIN-COUPLE	
DEFINITION	RECEPTOR LCRI HOMOLOG (HUMAN);, mRNA sequence.	
LOCUS	AA935648	
DEFINITION	93092805	
DEFINITION	AA935648.1 GI:3092805	
DEFINITION	EST.	
DEFINITION	human.	
DEFINITION	Homo sapiens	
DEFINITION	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
DEFINITION	Eutheria; Primates; Catarrhini; Homidae; Homo.	
DEFINITION	1 (bases 1 to 589)	
DEFINITION	NCI-CGAP http://www.nci.nlm.nih.gov/ncicgap .	
DEFINITION	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).	
DEFINITION	Tumor gene index	
DEFINITION	Unpublished (1997)	
DEFINITION	On Jan 17, 1998 this sequence version replaced gi:1900670.	

Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.lln.gov) for further information.
 Insert Length: 1009 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amersham
 High quality sequence stop: 511.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone IMAGE:1578064"
 /clone_11b="Soares_NFL_T_GBC.S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NDH19w, testis NHT, and B-cell
 NCI-GCAP-GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,

BASE COUNT 220 a 116 c 89 g 164 t
 ORIGIN

Query Match 33.9%; Score 589; DB 40; Length 589;
 Best Local Similarity 100.0%; Pred. No. 1.5e-97;
 Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1087 AAGCGAGTGCATTCATCTGTTCCACTGAGTGTGAGTCTTCAAGTTTCCACTCAGC 1146
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 589 AAGCGAGTGCATTCATCTGTTCCACTGAGTGTGAGTCTTCAAGTTTCCACTCAGC 530
 |||||
 1147 TAACACAGATGTAAAGACTTTTATACGATAAATACTTTTAAAGTACACAT 1206
 |||||
 529 TAACACAGATGTAAAGACTTTTATACGATAAATACTTTTAAAGTACACAT 470
 |||||
 1207 TTTTCAGATATAAAGACTGACCAATATTTGACAGTTTATGCTGTTGATTTTGT 1266
 |||||
 469 TTTTCAGATATAAAGACTGACCAATATTTGACAGTTTATGCTGTTGATTTTGT 410
 |||||
 1267 CTGTGTTCTTATGTTTGTGAGTTTAAATGACTTATTTAATAATTTTGT 1326
 |||||
 409 CTGTGTTCTTATGTTTGTGAGTTTAAATGACTTATTTAATAATTTTGT 350
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 1327 TCATATGATGTGTGTAGTAGCAGACCTGTGGCAAGTTCTTATGCTGTATGCTCG 1386
 |||||
 349 TCATATGATGTGTGTAGTAGCAGACCTGTGGCAAGTTCTTATGCTGTATGCTCG 290
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 1387 TGTAGAGACTGTAGAAAAGGAGACTGAACATTCACAGCCGTGTAGTAAACAGTAAAGC 1446
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 289 TGTAGAGACTGTAGAAAAGGAGACTGAACATTCACAGCCGTGTAGTAAACAGTAAAGC 230
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 1447 TAGAAATGATCCCGAGCTGTTATGACATATCTCCATCCCGTGGAGAGTTT 1506
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 229 TAGAAATGATCCCGAGCTGTTATGACATATCTCCATCCCGTGGAGAGTTT 170
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 1507 CCTGTCTTAAAGAGCTGTTTGTGTAGAAAGATGGCACTTATAACCAAGCCCAAGTG 1566
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 169 CCTGTCTTAAAGAGCTGTTTGTGTAGAAAGATGGCACTTATAACCAAGCCCAAGTG 110
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 1567 GTATAGAAATCTGCTGTTTTCAGTTTTCAGAGAGTGGTGTATTCAGACCTACAGTGA 1626
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 109 GTATAGAAATCTGCTGTTTTCAGTTTTCAGAGAGTGGTGTATTCAGACCTACAGTGA 50
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 1627 CAGCTCTTATTAAGTGTATATAAAGTACATGTTAAACTTAAAAA 1675
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 49 CAGCTCTTATTAAGTGTATATAAAGTACATGTTAAACTTAAAAA 1

RESULT 7
 AA411265 599 bp mRNA EST 17-MAY-1997
 LOCUS zv4h06.r1 Soares NHMPL SI Homo sapiens cDNA clone IMAGE:754619 5'
 DEFINITION similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1
 HOMOLOG (HUMAN); mRNA sequence.
 ACCESSION AA411265
 NID 92068847
 VERSION AA411265.1 GI:2068847
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 599)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
 Moore, B., Schellenberg, K., Stephe, M., Tan, F., Theisling, B.,
 White, Y., Wylie, T., Waterston, R. and Wilson, R.
 TITLE WashU-Merck EST Project 1997
 JOURNAL Unpublished (1997)
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1406946.

FEATURES
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 /clone="IMAGE:754619"
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 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: pTZ19-Pac
 (Pharmacia) with a modified polylinker; Site 1: Not I;
 Site 2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2bHM, pregnant uterus
 NBHPu, and fetal heart NBH19W) were mixed, and ss circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of 1 M.A.G.B. clones 260232-265223,
 340488-345479, and 484488-489479."

BASE COUNT 168 a 93 c 117 g 221 t
 ORIGIN

Query Match 32.7%; Score 567.8; DB 33; Length 599;
 Best Local Similarity 98.6%; Pred. No. 1e-93;
 Matches 583; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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 10 AAGCGAGTGCATTCATCTGTTCCACTGAGTGTGAGTCTTCAAGTTTCCACTCAGC 69
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 1147 TAACACAGATGTAAAGACTTTTATACGATAAATACTTTTAAAGTACACAT 1206
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 70 TAACACAGATGTAAAGACTTTTATACGATAAATACTTTTAAAGTACACAT 129
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 1207 TTTTCAGATATAAAGACTGACCAATATTTGACAGTTTATGCTGTTGATTTTGT 1266
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 130 TTTTCAGATATAAAGACTGACCAATATTTGACAGTTTATGCTGTTGATTTTGT 189
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 1267 CTGTGTTCTTATGTTTGTGAGTTTAAATGACTTATTTAATAATTTTGT 1326
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 130 CTGTGTTCTTATGTTTGTGAGTTTAAATGACTTATTTAATAATTTTGT 249
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 1327 TCATATGATGTGTGTAGTAGCAGACCTGTGGCAAGTTCTTATGCTGTATGCTCG 1386
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 250 TCATATGATGTGTGTAGTAGCAGACCTGTGGCAAGTTCTTATGCTGTATGCTCG 309
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 1387 TGTAGAGACTGTAGAAAAGGAGACTGAACATTCACAGCCGTGTAGTAAACAGTAAAGC 1446
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 310 TGTAGAGACTGTAGAAAAGGAGACTGAACATTCACAGCCGTGTAGTAAACAGTAAAGC 369
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 1507 CCTGTCTTAAAGAGCTGTTTGTGTAGAAAGATGGCACTTATAACCAAGCCCAAGTG 1566
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 430 CCTGTCTTAAAGAGCTGTTTGTGTAGAAAGATGGCACTTATAACCAAGCCCAAGTG 489
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 1567 GTATAGAAATCTGCTGTTTTCAGTTTTCAGAGAGTGGTGTATTCAGACCTACAGTGA 1626
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```

|||||
Db 490 GTATAGAAAGCTGTTTTCAGTTTCAGAGATGGGTGATTTCAGACCTACAGTGA 549
OY 1627 CAGCTCTGATTAAGTGTATATAAAGTACATGTATAACTTAAAAA 1677
Db 550 CAGCTTGATTAAGTGTATAT AAAGTACATGTATAAATAAAAAA 599

RESULT 8
AA576017/c 593 bp mRNA EST 09-SEP-1997
LOCUS AA576017/c
DEFINITION nm57604.s1 NCI-CGAP-Bc3 Homo sapiens cDNA clone IMAGE:1072327 3'
similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCRI
HOMOLOG (HUMAN): , mRNA sequence.
ACCESSION AA576017
NID 92350532
VERSION AA576017.1 GI:2350532
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 593)
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1405164.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrip/image/image.html

Insert Length: 1159 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 380.
Location/Qualifiers
1. 593
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1072327"
/clone_id="NCI-CGAP_Bc3"
/sex="female"
/tissue_type="breast tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: breast; Vector: Bluescript SK-; Site_1:
Ecorti; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Ductal breast tumor. 5' adaptor sequence: 5'
GAATTCGGCAGCAG 3' 3' adaptor sequence: 5'
CTCAGCTTTTCTTTTCTTTT 3' Average insert size: 0.9 kb."
BASE COUNT 220 a 117 c 95 g 161 t
ORIGIN

Query Match 31.5%; Score 546.8; DB 35; Length 593;
Best Local Similarity 99.5%; Pred. No. 6,6e-90;
Matches 559; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1108 GTTTCACCTAGTGTGCTCTTCAGTTTCTACGCCATACACAGATGTAAGACTT 1167
Db 561 GGTTCACCTAGTGTGCTCTCAAG-TTTCACCTCCAGCTAACCCAGATGTAAAAAGACTT 503
OY 1168 TTTTATACGATAAATAAGCTTTTATAGTTACACATTTTTCAGATATATAAGACTGA 1227
Db 502 TTTTATACGATAAATAAGCTTTTATAGTTACACATTTTTCAGATATATAAGACTGA 443

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OY 1228 CCAATATTGACAGTTTATTTGCTTGATTTTGTCTGTGTTCTTACTTTTG 1287
Db 442 CCAATATTGACAGTTTATTTGCTTGATTTTGTCTGTGTTCTTACTTTTG 383
OY 1288 TGAAGTTAATGACATATTATATATAATTTTGTCTTCATATTGATGTGTCTAGG 1347
Db 382 TGAAGTTAATGACATATTATATAATTTTGTCTTCATATTGATGTGTCTAGG 323
OY 1348 CAGACCTGTGGCCCAAGTTCTAGTCTGTATGTCGTGGTAGAGACTAGAAAAGG 1407
Db 322 CAGACCTGTGGCCCAAGTTCTAGTCTGTATGTCGTGGTAGAGACTAGAAAAGG 263
OY 1408 AACTGACATTCACAGACGCTAGTGAATACAGTAAGCTAGAAATGATCCCGCTGTT 1467
Db 262 AACTGACATTCACAGACGCTAGTGAATACAGTAAGCTAGAAATGATCCCGCTGTT 203
OY 1468 TATGATAGATATCTCTCATTCCTCGTGAACGTTTCTGTTCTTAAGACGTGATT 1527
Db 202 TATGATAGATATATCTCTCATTCCTCGTGAACGTTTCTGTTCTTAAGACGTGATT 143
OY 1528 TGTGTGAAAGANGGCACTTATTAACCAAGCCCAAGTGTATAGAAATGCTGTTTTC 1587
Db 142 TGTGTGAAAGANGGCACTTATTAACCAAGCCCAAGTGTATAGAAATGCTGTTTTC 83
OY 1588 AGTTTCAGGAGTGGTGTGATTCAGACCTACAGTGTAGTCTTATTAAGTTGTA 1647
Db 82 AGTTTCAGGAGTGGTGTGATTCAGACCTACAGTGTAGTCTTATTAAGTTGTA 23
OY 1648 ATAAAGTACATGTTAACTTA 1669
Db 22 ATAAAGTACATGTTAACTTA 1

RESULT 9
AA743645 556 bp mRNA EST 22-JAN-1998
LOCUS AA743645/c
DEFINITION ny24609.s1 NCI-CGAP GCBI Homo sapiens cDNA clone IMAGE:1272736 3'
similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCRI
HOMOLOG (HUMAN): , mRNA sequence.
ACCESSION AA743645
NID 92783151
VERSION AA743645.1 GI:2783151
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 556)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 9, 1998 this sequence version replaced gi:949470.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrip/image/image.html

Insert Length: 742 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 389.
Location/Qualifiers
1. 556

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 QY 1492 CCGTGGACGTTTTCTCTGTTCTTAAGACGATGTTTGGCTGAGACATGGCACTTTAA 1551
 |||||||
 Db 179 CCGTGGACGTTTTCTCTGTTCTTAAGACGATGTTTGGCTGAGACATGGCACTTTAA 120
 QY 1552 CCAAGGCCCAAGTGGATGAAATGCTGTTTTCAGTTTTCGAGGTGGGTGATTC 1611
 |||||||
 Db 119 CCAAGGCCCAAGTGGATGAAATGCTGTTTTCAGTTTTCGAGGTGGGTGATTC 60
 QY 1612 AGCACCACAGTGTACAGTCTGTATTAGTTGTTAATAAAGTACATGTTAACTTAA 1670
 |||||||
 Db 59 AGCACCACAGTGTACAGTCTGTATTAGTTGTTAATAAAGTACATGTTAACTTAA 1
 RESULT 11
 AA479467 521 bp mRNA EST 08-AUG-1997
 LOCUS z117f10.r1 Soares.NbHMPu.S1 Homo sapiens cDNA clone IMAGE:753931 5'
 DEFINITION similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCRI
 HOMOLOG (HUMAN);, mRNA sequence.
 AA479467
 NID 92208023
 VERSION AA479467.1 GI:2208023
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 521)
 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
 Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
 Moore,B., Schellenberg,K., Stepec,M., Tan,F., Theising,B.,
 White,Y., Wylie,T., Waterston,R. and Wilson,R.
 WashU-Merck EST Project 1997
 Unpublished (1997)
 On Sep 12, 1996 this sequence version replaced gi:1393144.
 TITLE JOURNAL
 COMMENT
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNCM; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 421.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /map="956G09:1"
 /clone_lib="Soares.NbHMPu.S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: pT713D-Pac
 (Pharmacia) with a modified polylinker; Site.1: Not I;
 Site.2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NMH, pregnant uterus
 NbHMPu, and fetal heart NbHMPu) were mixed, and ss circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of 1 M.A.G.E. clones 260232-265523,
 340488-345479, and 484488-489479."

BASE COUNT

132 a 104 c 103 g 182 t

ORIGIN
 Query Match 29.6%; Score 514.6; DB 34; Length 521;
 Best Local Similarity 99.2%; Pred. No. 4,4e-84;
 Matches 517; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 890 TGGAAATCATCAGCAGGGGTGAGTTGAGAACTGTGCAACTGTGCAATGATTCATCA 949
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 Db 1 TGGAAATCATCAGCAGGGGTGAGTTGAGAACTGTGCAACTGTGCAATGATTCATCA 60
 QY 950 CCGAGGCCCTAGCTTTCTTCTCAGCTGTGTGTAACCCATCTCTATAGCTTCTTGAG 1009
 |||||||
 Db 61 CCGAGGCCCTAGCTTTCTTCTCAGCTGTGTGTAACCCATCTCTATAGCTTCTTGAG 120
 QY 1010 CCAATTTTAAACCTCTGCCAGCAGCACTACCTCTGTGAGCAGAGGTCACAGCTCA 1069
 |||||||
 Db 121 CCAATTTTAAACCTCTGCCAGCAGCACTACCTCTGTGAGCAGAGGTCACAGCTCA 180
 QY 1070 AGATCCTCTCCAAAGGAAAGCAGAGGTGAGCATTCATCTGTTCACAGTGTGAGTCTT 1129
 |||||||
 Db 181 AGATCCTCTCCAAAGGAAAGCAGAGGTGAGCATTCATCTGTTCACAGTGTGAGTCTT 240
 QY 1130 CAAGTTTTCACCTCAGCTTAACAGATGTAAAGACTTTTATTATAGATAATAACTT 1189
 |||||||
 Db 241 CAAGTTTTCACCTCAGCTTAACAGATGTAAAGACTTTTATTATAGATAATAACTT 300
 QY 1190 TTTTATTAGTACACATTTTTCAGATATATAAGACTTACCAATATTGTACAGTTTATT 1249
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 Db 301 TTTTATTAGTACACATTTTTCAGATATATAAGACTTACCAATATTGTACAGTTTATT 360
 QY 1250 GCTTGTGAGATTTTGTCTGTCTGTCTTATGTTTGTGAGTTTAATGACTTATTTA 1309
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 Db 361 GCTTGTGAGATTTTGTCTGTCTGTCTTATGTTTGTGAGTTTAATGACTTATTTA 420
 QY 1310 TATAAATTTTGTGTTTTCATATTGATGTGTCTAGCAGAGCACTGTGCCAAGTTCTT 1369
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 Db 421 TATAAATTTTGTGTTTTCATATTGATGTGTCTAGCAGAGCACTGTGCCAAGTTCTT 480
 QY 1370 AGTTGCTGTATGTCGTGTGTAGGACTGTGAAAAGGGAAC 1410
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 Db 481 AGTTGCTGTATGTCGTGTGTAGGACTGTGAAAAGGGAAC 521
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 LOCUS nx85d08.s1 NCI-CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269039 3'
 DEFINITION similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCRI
 HOMOLOG (HUMAN);, mRNA sequence.
 AA747545
 NID 92787503
 VERSION AA747545.1 GI:2787503
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 555)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 On May 18, 1995 this sequence version replaced gi:811242.
 TITLE JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Louis M. Straub, M.D., Ph.D., David Allman,
 Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
www.bio.lnln.gov/dbtrp/Image/Image.html

Insert Length: 747 Std Error: 0.00
 Seq primer: -40ml3 fwd. Et from Amersham
 High quality sequence stop: 332.

FEATURES

Source

Location/Qualifiers

1..555
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 /map="20"
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 /clone_lib="NCI-CGAP-GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+ IgD-).
 Provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-GTTACCAATCTGAGTGGAGCGCGCCCTCATTTTCTTTTCTTTT-
 3']. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT733 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

210 a 108 c 84 g 153 t

ORIGIN

Query Match 29.5%; Score 511.8; DB 38; Length 555;
 Best Local Similarity 97.5%; Pred. No. 1.4e-83;
 Matches 541; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 1125 GCTTCAGTGTTCCTCCAGCTAA-CACAGATGTAAGAAAGACTTTTATACGATAA 1183
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 DB 555 GCTTCAAGTTTCTCCTCGCTAACCCGGTTTAAAGACTTTTATACGATAA 496
 QY 1184 TAACTTTTAAAGTACACATTTTTCAGATATAAAGACTGACATATGTACAGT 1243
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 DB 495 TAACTTTTAAAGTACACATTTTTCAGATATAAAGACTGACATATGTACAGT 436
 QY 1244 TTATTTGCTGTGGATTTTGTCTGTGTTCTTTAGTTTGTGAAGTTAATTGACT 1303
 |||||||
 DB 435 TTATTTGCTGTGGATTTTGTCTGTGTTCTTTAGTTTGTGAAGTTAATTGACT 376
 QY 1304 TATTTATATAATTTTGTTCATATGATGATGTCGTAGGAGACCTGTGGCAA 1363
 |||||||
 DB 375 TATTTATATAATTTTGTTCATATGATGATGTCGTAGGAGACCTGTGGCAA 316
 QY 1364 GTTCTAGTGTGATGTCGTGTGTAGAGACTGAGAAAGGAAGTGAACATTCAGA 1423
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 DB 315 GTTCTAGTGTGATGTCGTGTGTAGAGACTGAGAAAGGAAGTGAACATTCAGA 256
 QY 1424 GCGTGTAGTGAATCAGTAAGCTAGAAATGATCCCAAGCTGTTATGATGATTAATCT 1483
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 DB 255 GCGTGTAGTGAATCAGTAAGCTAGAAATGATCCCAAGCTGTTATGATGATTAATCT 196
 QY 1484 CTCGA-TCGCCGTGAGAGCTTTTCTGTCTTAAGAGCTGATTTTGGTGTGAAGATGG 1542
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 DB 195 CTCGAGTTCGCCGTGAGAGCTTTTCTGTCTTAAGAGCTGATTTTGGTGTGAAGATGG 136
 QY 1543 CACTATATACCAAAAGCCCAAGTGTATGAAATGCTGTTTTCAGTTTTCAGAGATGG 1602
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 DB 135 CACTATATACCAAAAGCCCAAGTGTATGAAATGCTGTTTTCAGTTTTCAGAGATGG 76
 QY 1603 GTTGAATTCAGACCTAGAGTGTACAGTCTTGTATTAAGTGTATAAAGTACATGTT 1662
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 DB 75 GTTGAATTCAGACCTAGAGTGTACAGTCTTGTATTAAGTGTATAAAGTACATGTT 16

QY 1663 AAACCTAAAAAAA 1677
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 DB 15 AAACCTAAAAAAA 1

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 DEFINITION
 AA148292 583 bp mRNA EST 06-AUG-1997
 z045e12.s1 Stragene endothelial cell 937223 Homo sapiens cDNA
 clone IMAGE:589870 3' similar to gb:L06797 PROBABLE G
 PROTEIN-COUPLED RECEPTOR LCRI HOMOLOG (HUMAN); mRNA sequence.

ACCESSION

AA148292

NID

G1717715

VERSION

AA148292.1 GI:1717715

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 583)

1 (bases 1 to 583)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
 Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,
 Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
 Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
 Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,
 and Maria, M.
 Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL
 MEDLINE
 Genome Res. 6 (9), 807-828 (1996)
 97044478
 On Sep 12, 1996 this sequence version replaced gi:1394539.

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (infoimage.lnln.gov) for further information.
 Insert Length: 888 Std Error: 0.00
 Seq primer: -40ml3 fwd. from Amersham
 High quality sequence stop: 386.

FEATURES

Source

Location/Qualifiers

1..383
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 /db_xref="taxon:9606"
 /clone="IMAGE:589870"
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 /dev_stage="umbilical vein, 1 passage"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; Cloned unidirectionally. Primer: Oligo dT.
 Umbilical vein endothelial cells, passaged once. Average
 insert size: 1.0 kb. Uni-ZAP XR Vector; -5' adaptor
 sequence: 5'-GAATTCGCGACGAG 3'-3' adaptor sequence: 5'-
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 CTGAGCTTTTCTTTTCTTTT 3-"
 BASE COUNT 212 a 119 c 90 g 160 t 2 others
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 Best Local Similarity 96.8%; Pred. No. 1.6e-82;
 Matches 569; Conservative 0; Mismatches 12; Indels 7; Gaps 5;

QY 1086 AAGGAGGTGACATCATCTGTTCCAGTCTGAGCTTCAGCTTTCAGTTCAGTTCAG 1145
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 DB 583 AAGGAGGTGACAT--CATCGTTCACAGAGTGC-GAGCTTCAAG-TTTCAGTTCAG 528
 |||||||
 QY 1146 CTACACAGAGTAAAGACTTTTATATGATTAATTAATCTTTTATTAAGTTACACA 1205
 |||||||

Db 527 CTACACGAGTGAAGGAGCT-TTTTATACGATAAATACTTTTTTTTAAAGTTACACA 469
 Qy 1206 TTTTTCAGATATAAAGCTACCAATATTTGACGTTTT--ATGCTGTGGATTTT 1263
 Db 468 TTTTTCAGATATAAAGCTACCAATATGTTACAGTTTNTATGTCCTTGTGGATTTT 409
 Qy 1264 TGCTGTGTTCTTCTTACTTTTGTGAAGTTAAATTCATTTATATATAATTTTTTTT 1323
 Db 408 TGCTGTGTTCTTCTTACTTTTGTGAAGTTAAATTCATTTATATATAATTTTTTTT 349
 Qy 1324 GTTTCATATTGATGTGTCTAGCGAGACCTGTGSCCAAGTTCTTAACTGTATGTC 1383
 Db 348 GTTTCATATTGATGTGTCTAGCGAGACCTGTGSCCAAGTTCTTAACTGTATGTC 289
 Qy 1384 TCGTGATGAGACTGAGAAAAAGGAACTGAACATTCAGAGCGGTAGTGAATCAGTAA 1443
 Db 288 TCGTGATGAGACTGAGAAAAAGGAACTGAACATTCAGAGCGGTAGTGAATCAGTAA 229
 Qy 1444 AGCTAGAAATGATCCCGACGCTGTTTATGCATAGATATCTCTCATTCCTCCGTGAACGTT 1503
 Db 228 AGCTAGAAATGATCCCGACGCTGTTTATGCATAGATATCTCTCATTCCTCCGTGAACGTT 169
 Qy 1504 TTTCTGTCTTTAAACGCTGATTTTGTGTGTAGTAAGATGGCACTTTAAACCAAGCCCAA 1563
 Db 168 TTTCTGTCTTTAAACGCTGATTTTGTGTGTAGTAAGATGGCACTTTAAACCAAGCCCAA 109
 Qy 1564 GTGATATGAAATGCTGCTTTTTCAGTTTTCAGAGTGGGTGATTTCAGCACTACAGT 1623
 Db 108 GTGATATGAAATGCTGCTTTTTCAGTTTTCAGAGTGGGTGATTTCAGCACTACAGT 49
 Qy 1624 GTACAGCTCTGTATTAGTTGTTAATAAAGTACATGTTAAACTTAA 1671
 Db 48 GTACAGCTCTGTATTAGTTGTTAATAAAGTACATGTTAAACTTAA 1

RESULT 14
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 LOCUS
 DEFINITION
 n=30h06.s1 NCI-CGAP-GC80 Homo sapiens CDNA clone IMAGE:1242011 3'
 similar to gb:106797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1
 HOMOLOG (HUMAN) ; mRNA sequence.
 AA804282
 NID 92873569
 VERSION AA804282.1 GI:2873569
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 536)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Jan 14, 1998 this sequence version replaced gi:11798484.

CONTACT: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
 Ph.D., Gerald Marti, M.D.
 CDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbtrp/image/image.html
 Insert Length: 1513 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 486.
 Location/Qualifiers
 1..536

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/organism="Homo sapiens"
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/map="21"
/clone_image="1242011"
/clone_id="NCI.CGAP.GCB0"
/tissue_type="germinal center B-cells"
/lab_host="SOLR (kanamycin resistant)"
/notes="Organ: tonsil; Vector: Bluescript SK-; Site: 1;
Ecobl: Site: 2; XhoI: Cloned 3' directionally. Primer:
0150 df. Germinal center B-cells Library constructed by
Dr. L. Staud (NCI). 3' adaptor sequence: 5'
GAATTCGGCAGCAG 3' 3' adaptor sequence: 5'
CTCAGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.1 kb."
BASE COUNT      195 a      107 c      81 g      153 t
ORIGIN
Query Match      28.9%; Score 501.2; DB 38; Length 536;
Best Local Similarity 98.1%; Pred. No. 1.2e-81;
Matches 528; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

OY 1141 TCCACCTAACAGATGTAAAGAACTTTTTTTTATACGATAAATACCTTTTTTAAGTT 1200
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 536 TCCACCTACGACAGATGTAAAGAAC-TGCTCTTATACATATAT-ACCTTTTTTTAAGTG 479
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1201 ACACATTTTTCAGATATAAAGACGTACCAATATGTACAGTTTTATTCGTTGGAT 1260
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 478 ACACATTTTCTCGATATATAAGACGTACCAATATGTACAGTTTTATTCGTTGGAT 419
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1261 TTTTGCTTTGTGTTCTTTAGTTTTTGGAAGTTAATTGACTTATTTATATAAATTTT 1320
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 418 TTTTGCTTTGTGTTCTTTAGTTTTTGGAAGTTAATTGACTTATTTATATAAATTTT 359
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1321 TTTGTTTCATATGATGTGTGCTAGGACGACCTGTGGCCAAGTCTTAGTTCGTGAT 1380
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 358 TTTGTTTCATATGATGTGTGTAGGACGACCTGTGGCCAAGTCTTAGTTCGTGAT 299
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1381 GTCTGTGTGTAGGACTGTAGAAAAGGAAGTCAACATTCCAGAGCGTAGTGAATCACG 1440
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 298 GTCTGTGTGTAGGACTGTAGAAAAGGAAGTCAACATTCCAGAGCGTAGTGAATCACG 239
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1441 TAAAGCTGAATATGATCCCGACGCTTTATATGATATGATCTCTCCATCCCGGTGAAC 1500
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 238 TAAAGCTGAATATGATCCCGACGCTTTATATGATATGATCTCTCCATCCCGGTGAAC 179
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1501 GTTTTCTGTTCTTAAAGCGTGAATTTTGCTGTAGAGATGCGACTATATACCAAGCCC 1560
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 178 GTTTTCTGTTCTTAAAGCGTGAATTTTGCTGTAGAGATGCGACTATATACCAAGCCC 119
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1561 AAAGGTGATATGAATATGCGGTTTTTCAGGTTTTCAGAGAGTGGGTGATTTCGCACTAC 1620
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 118 AAAGGTGATATGAATATGCGGTTTTTCAGGTTTTCAGAGAGTGGGTGATTTCGCACTAC 59
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1621 AGTGTACAGTCTTGATTAAGTTGTTAATAAAGTACATGTTAAACTTAAAAAATAA 1678
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 58 AGTGTACAGTCTTGATTAAGTTGTTAATAAAGTACATGTTAAACTTAAAAAATAA 1
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
LOCUS      AA426644/C
DEFINITION AA426644 501 bp mRNA EST 16-OCT-1997
            z47h11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:756637 3', similar to gb:U06797 PROBABLE G PROTEIN-COUPLED
            RECEPTOR LCRI HOMOLOG (HUMAN)), mRNA sequence.
ACCESSION  AA426644
VERSION    92107314
KEYWORDS   AA426644.1 GI:2107314
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 501)

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